

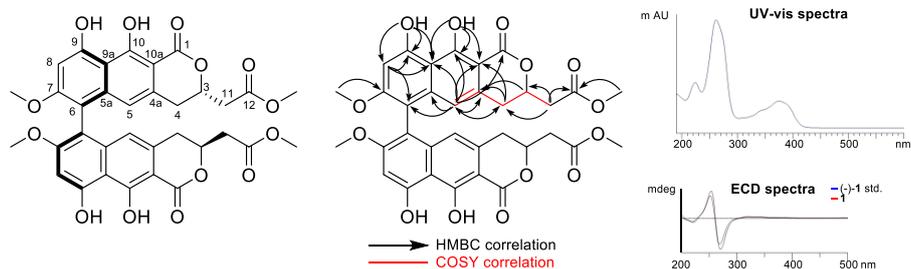
**Table S1. Genome sequencing statistics for the assembly of *Aspergillus viridinutans* strain FRR 0576.** The assembly and raw reads are available from GenBank under BioProject PRJNA513223.

Number of contigs	285
Median length (bp)	5,707
Mean length (bp)	104,615
Max length (bp)	1,359,167
N50 length (bp)	425,947
Number of contigs >N50	21
Length sum (bp)	29,815,307

**Table S2. Protein IDs and features of the *Vdt* cluster genes in *Paecilomyces variotii* strains CBS 101075 and CBS 144490.**

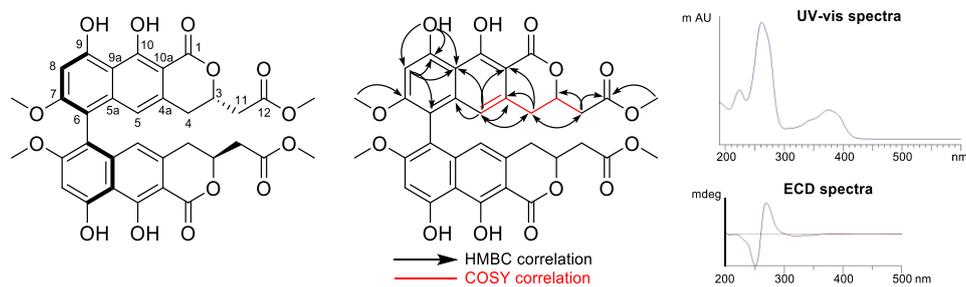
Protein	Protein ID CBS 101075	Protein ID CBS 144490	Putative function	Similarity/query cover to homologs discussed in the main text
VdtA	480069	260870	Polyketide synthase	42/94% to PKS12 ( <i>F. graminearum</i> ; aurofusarin)
VdtB	480050	260889	Laccase	53/86% to GIP1 ( <i>F. graminearum</i> ; aurofusarin)
VdtC	488617	127223	<i>O</i> -methyltransferase	44/96% to AurJ ( <i>F. graminearum</i> ; aurofusarin)
VdtD	510289	190631	Hydrolase-like	N/A
VdtE	480056	190779	Baeyer-Villiger monooxygenase	26/87% to MoxY ( <i>A. parasiticus</i> ; aflatoxin)
VdtF	480057	260883	Reductase	29/91% to FabG ( <i>E. coli</i> )
VdtG	488624	275282	Major facilitator superfamily transporter	49/89% to AurT ( <i>F. graminearum</i> ; aurofusarin)
VdtR	105452	288289	Transcription factor	39/37% to AurR1 ( <i>F. graminearum</i> ; aurofusarin)
VdtX	515060	190767	PKS-like	37/97% to Fum1 ( <i>Fusarium verticillioides</i> )

**Table S3. Structural information of 1 (chloroform-*d*).**



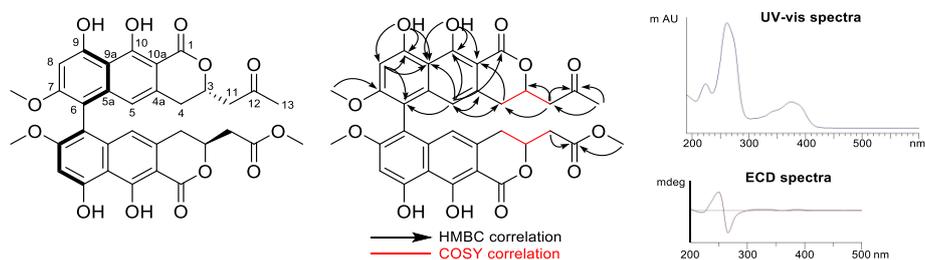
Carbon No.	<sup>13</sup> C NMR	<sup>1</sup> H NMR (ppm, multi, <i>J</i> )	gCOSY	HMBC
1	171.0	-	-	-
2	-	-	-	-
3	75.9	4.96 (1H, m)	4, 11	4a
4	33.0	2.81 (2H, m)	3, 5	4a, 5, 10a
4a	132.1	-		-
5	114.2	6.23 (1H, s)	4	1, 3, 4a, 5a, 6, 9a, 10, 10a
5a	139.3	-	-	-
6	110.1	-	-	-
7	161.2	-	-	-
7-OMe	56.3	3.77 (3H, s)	-	7
8	98.4	6.79 (1H, s)	-	6, 9, 9a
9	159.3	-	-	-
9-OH	-	9.69 (1H, s)	-	8, 9, 9a
9a	108.1	-	-	-
10	163.5	-	-	-
10-OH	-	13.75 (1H, s)	-	9a, 10, 10a
10a	98.8	-	-	-
11	39.5	2.65 (1H, dd, <i>J</i> =7.74, 19.5) 2.88 (1H, dd, <i>J</i> =8.16, 19.4)	4	3, 4, 12
12	169.8	-	-	-
12-OMe	52.2	3.70 (3H, s)	-	12

**Table S4. Structural information of 1' (chloroform-*d*).**



Carbon No.	<sup>13</sup> C NMR	<sup>1</sup> H NMR (ppm, multi, <i>J</i> )	gCOSY	HMBC
1	171.1	-	-	-
2	-	-	-	-
3	75.9	4.96 (1H, m)	4, 11	-
4	32.9	2.87 (2H, m)	3, 5	4a, 5, 10a, 11
4a	132.1	-	-	-
5	114.2	6.24 (1H, s)	4	4, 4a, 5a, 9a, 10a
5a	139.4	-	-	-
6	110.2	-	-	-
7	161.2	-	-	-
7-OMe	56.3	3.75 (3H, s)	-	7
8	98.3	6.79 (1H, s)	-	6, 9, 9a
9	159.3	-	-	-
9-OH	-	9.77 (1H, s)	-	8, 9, 9a
9a	108.2	-	-	-
10	163.6	-	-	-
10-OH	-	13.77 (1H, s)	-	-
10a	98.9	-	-	-
11	39.5	2.68 (1H, dd, <i>J</i> =6.55, 16.3) 2.92 (1H, dd, <i>J</i> = 6.70, 16.3)	4	3, 4, 12
12	169.9	-	-	-
12-OMe	52.3	3.70 (3H, s)	-	12

**Table S5. Structural information of 2 (acetonitrile-*d*<sub>3</sub>).**

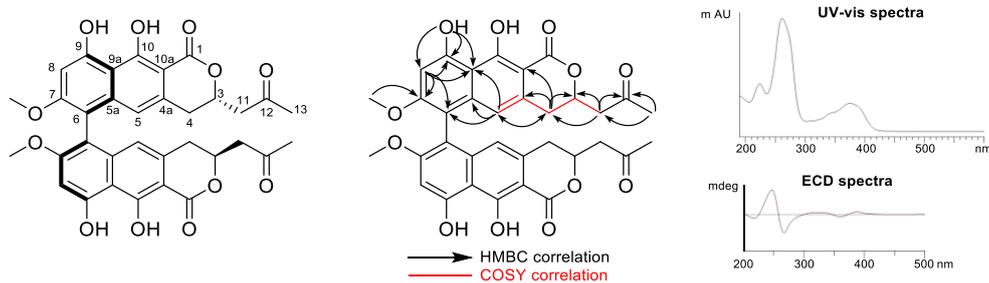


Carbon No.	<sup>13</sup> C NMR	<sup>1</sup> H NMR (ppm, multi, <i>J</i> )	gCOSY	HMBC
1	172.2	-	-	-
1'	172.0	-	-	-
2 (2')	-	-	-	-
3	76.8	4.96 (2H, m)	4, 11	-
3'	77.3	4.96 (2H, m)	4', 11'	-
4	32.8	2.68 <sup>[a]</sup>	3	5, 10a
4'	33.0	2.68 <sup>[a]</sup>	3'	5', 10a'
4a	134.2	-	-	-
4a'	134.0	-	-	-
5	114.8	6.28 (2H, s)	-	1, 4, 4a, 6, 9a, 10
5'	114.7	6.28 (2H, s)	-	1', 4', 4a', 6', 9a', 10'
5a (5a')	140.1	-	-	-
6 (6')	110.9	-	-	-
7 (7')	161.8	-	-	-
7 (7')-OMe	56.8	3.71 (6H, s)	-	7 (7')
8 (8')	99.0	6.83 (1H, s)	-	6 (6'), 9 (9'), 9a (9a')
9 (9')	159.9	-	-	-
9 (9')-OH	-	9.68 (2H, s)	-	8 (8'), 9 (9'), 9a (9a')
9a (9a')	108.5	-	-	-
10	163.7	-	-	-
10'	163.8	-	-	-
10 (10')-OH	-	13.8 (1H, s)	-	9a (9a'), 10 (10'), 10a (10a')
10a	100.0	-	-	-
10a'	99.9	-	-	-
11	48.3	2.96 (1H, dd, <i>J</i> =7.65, 17.4) 2.74 <sup>[a]</sup>	3	3, 4, 12
11'	39.9	2.70 <sup>[a]</sup>	3'	3', 4', 12'
12	205.7	-	-	-

12'	170.9	-	-	-
13	30.6	2.12 (3H, s)	-	11, 12
12'-OMe	52.4	3.65 (3H, s)	-	12'

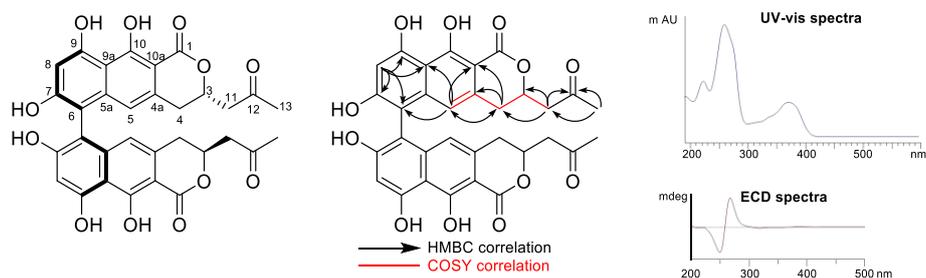
[a] unable to integrate or calculate *J* due to signal overlay

**Table S6. Structural information of 3 (acetonitrile-*d*<sub>3</sub>).**



Carbon No.	<sup>13</sup> C NMR	<sup>1</sup> H NMR (ppm, multi, <i>J</i> )	gCOSY	HMBC
1	172.2	-	-	-
2	-	-	-	-
3	76.8	4.98 (1H, m)	4, 11	-
4	33.0	2.79 (2H, m)	3, 5	3, 4a, 5, 10a
4a	134.4	-	-	-
5	114.7	6.27 (1H, s)	4	4, 5a, 6, 9a
5a	140.2	-	-	-
6	110.9	-	-	-
7	161.8	-	-	-
7-OMe	56.8	3.71 (3H, s)	-	7
8	99.0	6.84 (1H, s)	-	6, 7, 9, 9a
9	159.9	-	-	-
9-OH	-	9.73 (1H, s)	-	8, 9, 9a
9a	108.6	-	-	-
10	163.8	-	-	-
10-OH	-	13.84 (1H, s)	-	-
10a	100.1	-	-	-
11	48.3	2.76 (1H, dd, <i>J</i> =7.92, 17.5) 2.96 (1H, dd, <i>J</i> =7.74, 17.5)	4	3, 4, 12
12	205.7	-	-	-
13	30.6	2.11 (3H, s)	-	11, 12

**Table S7. Structural information of 4 (acetonitrile-*d*<sub>3</sub>).**



Carbon No.	<sup>13</sup> C NMR	<sup>1</sup> H NMR (ppm, multi, <i>J</i> )	gCOSY	HMBC
1	172.2	-	-	-
2	-	-	-	-
3	76.8	4.92 (1H, m)	4, 11	-
4	33.1	2.79 <sup>[a]</sup>	3, 5	4a, 5, 10a
4a	135.0	-	-	-
5	114.4	6.35 (1H, s)	4	4, 9a, 10a
5a	141.5	-	-	-
6	109.2	-	-	-
7	160.5	-	-	-
7-OH	-	-	-	-
8	102.7	6.60 (1H, s)	-	6, 7, 9, 9a
9	160.0	-	-	-
9-OH	-	-	-	-
9a	107.0	-	-	-
10	163.6	-	-	-
10-OH	-	-	-	-
10a	100.3	-	-	-
11	48.3	2.78 <sup>[a]</sup> 2.95 (1H, dd, <i>J</i> =7.45, 17.45)	3	3, 4, 12
12	205.9	-	-	-
13	30.6	2.11 (3H, s)	-	11, 12

[a] unable to integrate or calculate *J* due to signal overlay

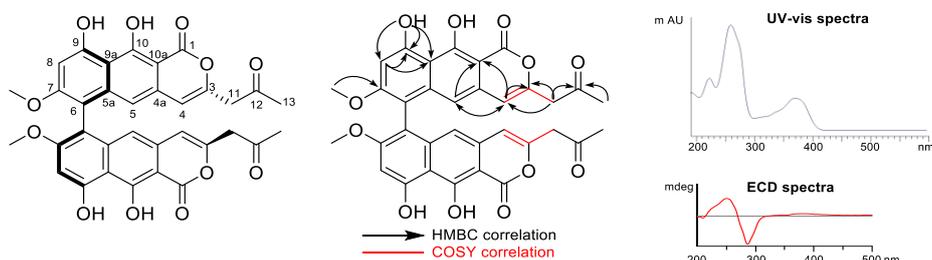
**Table S8. Structural information of 5 (acetonitrile-*d*<sub>3</sub>).**

Carbon No.	<sup>13</sup> C NMR	<sup>1</sup> H NMR (ppm, multi, <i>J</i> )	gCOSY	HMBC
1	172.2	-	-	-
1'	172.0	-	-	-
2 (2')	-	-	-	-
3	76.8	4.89 (1H, m)	4, 11	-
3'	77.3	4.89 (1H, m)	4', 11'	-
4	33.0	2.81 <sup>[a]</sup>	3	4a, 5, 10a
4'	32.8	2.81 <sup>[a]</sup>	3'	4a', 5', 10a'
4a	135.0	-	-	-
4a'	134.7	-	-	-
5	114.5	6.36 (1H, s)	-	4, 5a, 6, 9a, 10, 10a
5'	114.4	6.36 (1H, s)	-	4', 5a', 6', 9a', 10', 10a'
5a (5a')	141.5	-	-	-
6 (6')	106.9	-	-	-
7 (7')	160.5	-	-	-
7 (7')-OH	-	-	-	-
8 (8')	102.7	6.60 (1H, s)	-	6 (6'), 7 (7'), 9 (9'), 9a (9a')
9 (9')	160.0	-	-	-
9 (9')-OH	-	-	-	-
9a (9a')	109.2	-	-	-
10	163.5	-	-	-
10'	163.6	-	-	-
10 (10')-OH	-	-	-	-
10a	100.0	-	-	-
10a'	99.9	-	-	-
11	48.3	2.74 <sup>[a]</sup> 2.96 (1H, dd, <i>J</i> =7.44, 17.52)	3	3, 4, 12
11'	39.9	2.70 <sup>[a]</sup>	3'	3', 4', 12'
12	205.7	-	-	-

12'	170.0	-	-	-
13	30.6	2.10 (1.5H, s)	-	11, 12
12'-OMe	52.5	3.62 (1.5H, s)	-	12'

[a] unable to integrate or calculate *J* due to signal overlay

**Table S9. Structural information of 7 (chloroform-*d*).**

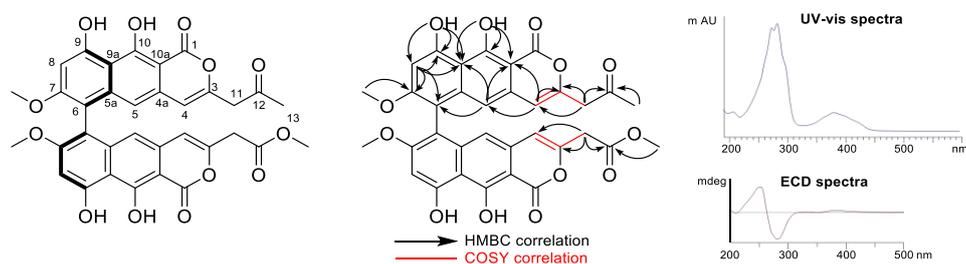


Carbon No.	<sup>13</sup> C NMR	<sup>1</sup> H NMR (ppm, multi, <i>f</i> )	gCOSY	HMBC
1	168.0 <sup>[a]</sup>	-	-	-
2	-	-	-	-
3	148.4	-	-	-
4	108.3	6.10 (1H, s) <sup>l</sup>	11	3, 5, 10a
4a	- <sup>[b]</sup>	-	-	-
5	111.7	6.36 (1H, s)	-	4, 10a
5a	140.2 <sup>[a]</sup>	-	-	-
6	109.9 <sup>[a]</sup>	-	-	-
7	161.3	-	-	-
7-OMe	56.4	3.77 (3H, s)	-	7
8	98.4	6.84 (1H, s)	-	9, 9a
9	159.3	-	-	-
9-OH	-	9.75(1H, s)	-	8, 9, 9a
9a	- <sup>[b]</sup>	-	-	-
10	163.0 <sup>[a]</sup>	-	-	-
10-OH	-	13.6 (1H, s)	-	-
10a	97.5	-	-	-
11	47.6	3.47 (2H, s)	4	3, 4, 12
12	202.2	-	-	-
13	30.1	2.23 (3H, s)	-	12

[a] Lacking HMBC correlations. Chemical shifts assigned based on other compounds isolated.

[b] <sup>13</sup>C signals not detected.

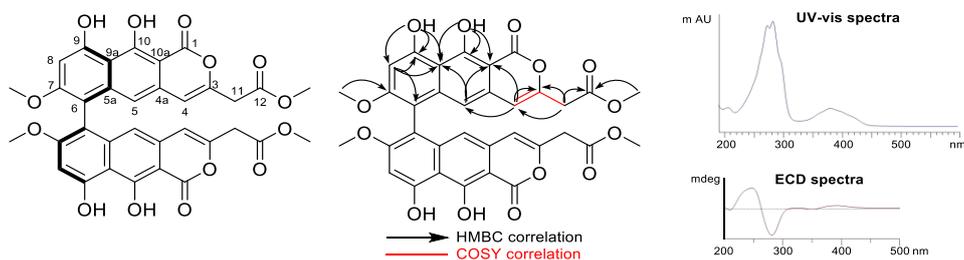
**Table S10. Structural information of 8 (chloroform-*d*).**



Carbon No.	<sup>13</sup> C NMR	<sup>1</sup> H NMR (ppm, multi, <i>J</i> )	gCOSY	HMBC
1	.168.0	-	-	-
1'	167.9	-	-	-
2 (2')	-	-	-	-
3	148.4	-	-	-
3'	147.9	-	-	-
4	108.3	6.10 (1H, s)	11	3, 5, 10a
4'	108.0	6.15 (1H, s)	11'	3', 5', 10a'
4a	130.2	-	-	-
4a'	130.5	-	-	-
5	111.7	6.36 (1 H, s)	-	6, 9a, 10a
5'	111.8	6.37 (1 H, s)	-	6', 9a', 10a'
5a (5a')	140.2	-	-	-
6 (6')	109.9	-	-	-
7 (7')	161.3	-	-	-
7 (7')-OMe	56.4	3.77 (6H, s)	-	7 (7')
8 (8')	98.4	6.84 (2H, s)	-	6 (6'), 7 (7'), 9 (9'), 9a (9a')
9 (9')	159.3	-	-	-
9 (9')-OH	-	9.75 (2H, s)	-	8 (8'), 9 (9'), 9a (9a')
9a (9a')	108.2	-	-	-
10 (10')	163.0	-	-	-
10 (10')-OH	-	13.6 (2H, s)	-	9a (9a'), 10 (10a'), 9a (9a')
10a	97.5	-	-	-
10a'	97.6	-	-	-
11	47.6	3.47 (2H, s)	4	3, 4, 12
11'	38.8	3.43 (2H, s)	4'	3', 4', 12'
12	202.2	-	-	-
12'	168.7	-	-	-

13	30.1	2.23 (3H, s)	-	12
12'-OMe	52.7	3.71 (3H, s)	-	12'

**Table S11. Structural information of 9 (chloroform-*d*).**



Carbon No.	<sup>13</sup> C NMR	<sup>1</sup> H NMR (ppm, multi, <i>f</i> )	gCOSY	HMBC
1	167.9 <sup>[a]</sup>	-	-	-
2	-	-	-	-
3	147.9	-	-	-
4	108.0	6.15 (1H, s)	11	3, 5, 10a
4a	130.8 <sup>[a]</sup>	-	-	-
5	111.8	6.37 (1H, s)	-	9a, 10a
5a	140.2 <sup>[a]</sup>	-	-	-
6	110.0 <sup>[a]</sup>	-	-	-
7	161.2	-	-	-
7-OMe	56.4	3.77 (3H, s)	-	7
8	98.5	6.84 (1H, s)	-	6, 9, 9a
9	159.3	-	-	-
9-OH	-	9.69	-	8, 9, 9a
9a	108.1	-	-	-
10	163.0	-	-	-
10-OH	-	13.75	-	9a, 10, 10a
10a	97.6	-	-	-
11	38.8	3.43 (2H, s)	4	3, 4, 12
12	168.7	-	-	-
12-OMe	52.7	3.71(3H, s)	-	12

[a] <sup>13</sup>C signals have no HMBC correlations. The chemical shifts were assigned based on data of other compounds.

**Table S12. Oligonucleotide primers designed in this study**

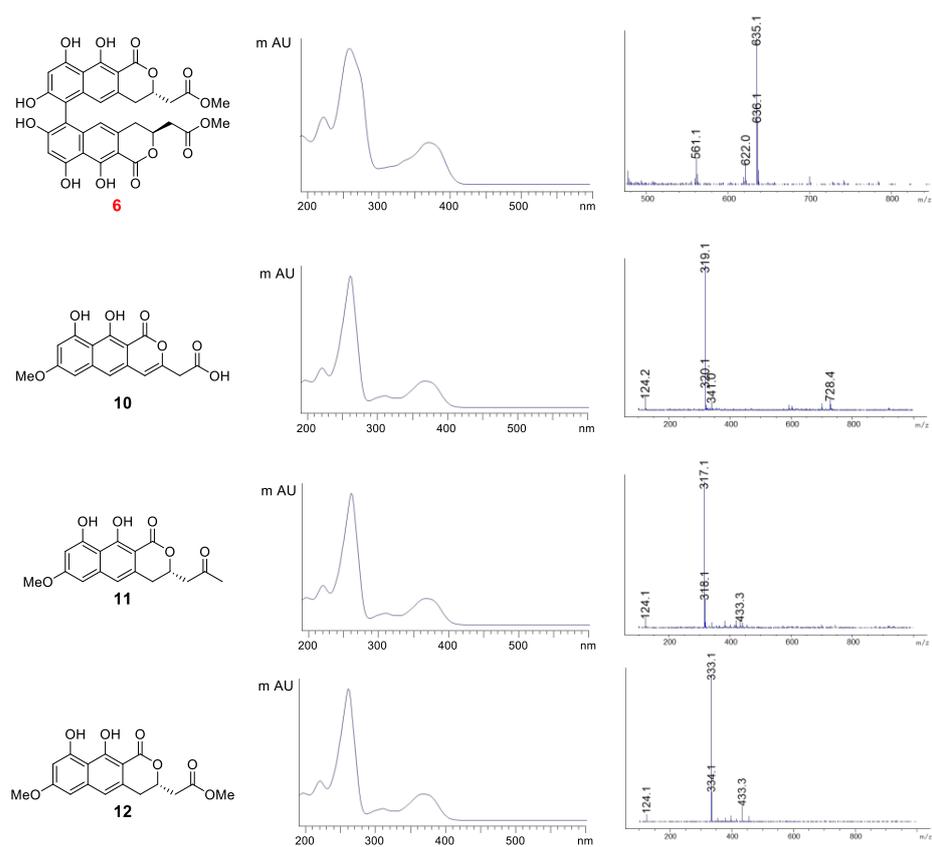
Name	Sequence (5' to 3')	Notes
<i>vdtB5'F</i>	AACAGCTATGACATGATTACGAATCGACGTTGTTTCTTGG	Primers used to amplify 5' flank of <i>vdtB</i>
<i>vdtB5'R</i>	GTGGGCAGAATTCGCTCCATGGCAGCAATGTCC	
<i>vdtC5'F</i>	AACAGCTATGACATGATTACGTGCTTCTTTATACTGGGTCG	Primers used to amplify 5' flank of <i>vdtC</i>
<i>vdtC5'R</i>	TTGAAGAGAATTCGAAGCACTGATTGCCTGTGC	
<i>vdtD5'F</i>	AACAGCTATGACATGATTACGCCTTCTTCAAGTATCTTTCC	Primers used to amplify 5' flank of <i>vdtD</i>
<i>vdtD5'R</i>	ACATACGGAATTCTGGTAACGGAAGGAAAAGACC	
<i>vdtE5'F</i>	AACAGCTATGACATGATTACGGGTTTGTAGGGATCGAATG C	Primers used to amplify 5' flank of <i>vdtE</i>
<i>vdtE5'R</i>	CCGAAGGGAATTCCAACCTCTGAAATACATCTCC	
<i>vdtF5'F</i>	AACAGCTATGACATGATTACGCGTCAATCGAGTTGAAATG G	Primers used to amplify 5' flank of <i>vdtF</i>
<i>vdtF5'R</i>	CAGTCGAGAATTCGTCTGTTCTGTTGTTGGTGC	
<i>vdtG5'F</i>	AACAGCTATGACATGATTACGGGTCTGTTCTGTTGTTGGTG C	Primers used to amplify 5' flank of <i>vdtG</i>
<i>vdtG5'R</i>	CCTCAGGGAATTCTGATCGAGCGCCAACCTACC	
<i>vdtA5'F</i>	AACAGCTATGACATGATTACGTTCTTATATACTTATAATTC G	Primers used to amplify 5' flank of <i>vdtA</i>
<i>vdtA5'R</i>	GAGAACGGGATCCATAAACGACGCAAGCTGG	
<i>vdtR5'F</i>	AACAGCTATGACATGATTACGGCGTGCGTAGTAGCTGCTG C	Primers used to amplify 5' flank of <i>vdtR</i>
<i>vdtR5'R</i>	AGATTGGAATTCTTGAGATAGGGTTTGACTGG	
<i>vdtB3'F</i>	ATGGAGCGAATTCTGCCACGGAGACGATATGC	Primers used to amplify 3' flank of <i>vdtB</i>
<i>vdtB3'R</i>	GTAAAACGACGGCCAGTGCCAGGGCACACAAAGAATCTAG G	
<i>vdtC3'F</i>	GTGCTTCGAATTCTTCAAGTATCTTTCCAGC	Primers used to amplify 3' flank of <i>vdtC</i>
<i>vdtC3'R</i>	GTAAAACGACGGCCAGTGCCAGGTAACGGAAGGAAAAGA CC	
<i>vdtD3'F</i>	GTTACCAGAATTCCGTATGTCTTTAATGAGTTGG	Primers used to amplify 3' flank of <i>vdtD</i>
<i>vdtD3'R</i>	GTAAAACGACGGCCAGTGCCAATAATAATGTATCCGCTAG G	
<i>vdtE3'F</i>	AGAGTTGGAATTCCCTTCGGAGGAAAACGTACC	Primers used to amplify 3' flank of <i>vdtE</i>
<i>vdtE3'R</i>	GTAAAACGACGGCCAGTGCCAATGCTAATATTCTGCCCTGC	
<i>vdtF3'F</i>	AACAGACGAATTCTCGACTGCCTGCTTCACTGG	Primers used to amplify 3' flank of <i>vdtF</i>
<i>vdtF3'R</i>	GTAAAACGACGGCCAGTGCCAGGCTTCGACACAAACACTG G	
<i>vdtG3'F</i>	TCGATCAGAATTCCTGAGGGGAGGAAACAAGG	Primers used to amplify 3' flank of <i>vdtG</i>
<i>vdtG3'R</i>	GTAAAACGACGGCCAGTGCCAGCCCAGCCCATTACTGCAG C	
<i>vdtA3'F</i>	CGTTTATGGATCCCGTTCTCATTCCGGTACAGC	Primers used to amplify 3' flank of <i>vdtA</i>
<i>vdtA3'R</i>	GTAAAACGACGGCCAGTGCCAAAAGGGGTGGATAATAA	

	GC	
<i>vdtR3'F</i>	TATCTCAAGAATTCCAATCTGCCCTCGAGTACG	Primers used to amplify 3' flank of <i>vdtR</i>
<i>vdtR3'R</i>	GTA AACGACGGCCAGTGCCAGTGCATTTCTTATACTCAAG G	
<i>vdtBHYGF</i>	GGACATTGCTGCCATGGAGCGCTGGGATTGCCCCCTCGATGC	Primers used to amplify HYG cassette for introduction into the <i>vdtB</i> construct
<i>vdtBHYGR</i>	GCATATCGTCTCCGTGGGCAGCCTACTGAACGTTATGAC	
<i>vdtCHYGF</i>	CACAGGCAATCAGTGCTTCGCTGGGATTGCCCCCTCGATGC	Primers used to amplify HYG cassette for introduction into the <i>vdtC</i> construct
<i>vdtCHYGR</i>	CTGGAAAGATACTTGAAGAGCCTACTGAACGTTATGAC	
<i>vdtDHYGF</i>	TCTTTTCCTTCCGTTACCAGCTGGGATTGCCCCCTCGATGC	Primers used to amplify HYG cassette for introduction into the <i>vdtD</i> construct
<i>vdtDHYGR</i>	AACTCATTAAGACATACGGCCTACTGAACGTTATGAC	
<i>vdtEHYGF</i>	GAGATGTATTTAGAGTTGGCTGGGATTGCCCCCTCGATGC	Primers used to amplify HYG cassette for introduction into the <i>vdtE</i> construct
<i>vdtEHYGR</i>	GTACGTTTTCTCCGAAGGGCCTACTGAACGTTATGAC	
<i>vdtFHYGF</i>	CACCAACAACAGAACAGACGCTGGGATTGCCCCCTCGATGC	Primers used to amplify HYG cassette for introduction into the <i>vdtF</i> construct
<i>vdtFHYGR</i>	CAGTGAAGCAGGCAGTCGAGCCTACTGAACGTTATGAC	
<i>vdtGHYGF</i>	GTAGGTTGGCGCTCGATCAGCTGGGATTGCCCCCTCGATGC	Primers used to amplify HYG cassette for introduction into the <i>vdtG</i> construct
<i>vdtGHYGR</i>	CTTGTTTCCTCCCTCAGGGCCTACTGAACGTTATGAC	
<i>vdtAHYGF</i>	CCAGCTTGCCTCGTTTATGCTGGGATTGCCCCCTCGATGC	Primers used to amplify HYG cassette for introduction into the <i>vdtA</i> construct
<i>vdtAHYGR</i>	GCTGTACCGAATGAGAACGGCCTACTGAACGTTATGAC	
<i>vdtRHYGF</i>	CCAGTCAAACCCTATCTCAAGCTGGGATTGCCCCCTCGATGC	Primers used to amplify HYG cassette for introduction into the <i>vdtR</i> construct
<i>vdtRHYGR</i>	CGTACTCGAGGGCAGATTGCCTACTGAACGTTATGAC	
AP124	AGTCGGCTGTTTGCATCTGC	488617ScF
AP125	GATCTGGGTCATAAACATCG	488617ScR
AP126	GAGGAGCAAGACAGAGACGG	510289scF
AP127	CTTGCATACTTGCCATTTTGG	510289scR
AP128	ATCATTGGGGAGATGGGAGG	480056ScF
AP129	GGTTATGTGTCGAATAAGCC	480056ScR
AP130	TGCCGTACCAACCGATATCG	480057scF
AP131	ATGTGATCATTCTAGCGACC	480057scR

AP132	CGGTTAATGCTTTTCCATCC	488624scF
AP133	TTTCTCTGATAGGACGATCC	488624scR
AP134	AATTGAGAGATTAGATAGCG	480069scF
AP135	GCAGATGGAGGAGCCATAGC	480069scR
AP136	TGGATGTCTTCCGGGTGCG	105452_ScF
AP137	TTATTATGTGACACGTCTCG	105452_ScR
AP138	CAGCTTGATTCCTCTGCC	480050ScF
AP139	TATAGGGGGGACCTTCAACC	480050ScR
<b>qPCR primers</b>		
<b>Name</b>	<b>Sequence (5' to 3')</b>	<b>Notes</b>
<i>vdtBqPCRf</i>	CTATCACAGACAAAGGGTGC	qPCR primers for <i>vdtB</i>
<i>vdtBqPCRr</i>	AGGGAACACAGCCTTCCTGG	
<i>vdtCqPCRf</i>	GCGATCGTGGTTGATGTTGG	qPCR primers for <i>vdtC</i>
<i>vdtCqPCRr</i>	TCACCATGGGCAGGTCTTGC	
<i>vdtDqPCRf</i>	ACGGGTTCCGCGCATTATGC	qPCR primers for <i>vdtD</i>
<i>vdtDqPCRr</i>	AGGATAGATATATTGGCTGG	
<i>vdtEqPCRf</i>	GAGCCGTTGAATTGGTTTGG	qPCR primers for <i>vdtE</i>
<i>vdtEqPCRr</i>	AAGACCGAAGAGAATATTC	
<i>vdtFqPCRf</i>	CATCTACGGTGCAGTAAGG	qPCR primers for <i>vdtF</i>
<i>vdtFqPCRr</i>	ATGTCGGTGTGAAATATCC	
<i>vdtGqPCRf</i>	AGGATGCGGAATGAGCATGC	qPCR primers for <i>vdtG</i>
<i>vdtGqPCRr</i>	AAGAAGATGAGCGAGATACC	
<i>vdtX1qPCRf</i>	AGAGAGTAAACGTCTGTTGG	qPCR primers for <i>vdtX</i>
<i>vdtXqPCRr</i>	GCATTGTCGGATATCCGTCG	
<i>vdtAqPCRf</i>	AGCGACGGACAGATTTCTCG	qPCR primers for <i>vdtA</i>
<i>vdtAqPCRr</i>	TATAGGGTTCCTCCTGCAGC	
<i>β-tubulinqPCRf</i>	GGGCGAGGAGGAGTACAACG	qPCR primers for β-tubulin
<i>β-tubulinqPCRr</i>	AATGGGGTATTACTGAGAGC	
<i>ID423248qPCRf</i>	AGAGGATGGATTCAGAGAGC	qPCR primers for protein ID423248
<i>ID423248qPCRr</i>	GCAACGCGCGACGTTCTTCC	
AP169	TAAGGGCGATGATGTATTGG	qPCR primers for protein ID510298
AP170	GTCAGTAGGCGTCGATCTGC	
AP171	CCTGTGCTTTCTATAATGACC	qPCR primers for protein ID480071
AP172	CGTGATTCTGAAGGAGTGC	
<b>Fluorescent tagging primers</b>		
<b>Name</b>	<b>Sequence (5' to 3')</b>	
24GFP5F	AACAGCTATGACATGATTACGTATTCTGCTCTTCTTGAACC	
24GFP5R	GCTCCTCGCCCTTGCTCACTACCTTGTTTCCTCCCCTCAGG	
24GFP6FPF	GTGAGCAAGGGCGAGGAGC	
24GFP6FPR	TAAAACGACGGCCAGTGCCAGAATTCGGTTGTTGGTGCTGGTGG	
24GFPHYGF	CACCAGCACCAACAACCGCTGGGATTGCCCTCGATGC	
24GFPHYGR	GCTTACTATACATGCATATTTCTACTGAACGTTATGAC	

24GFP3F	AAATATGCATGTATAGTAAGC	
24GFP3R	AAAACGACGGCCAGTGCCAGGCCAGCCCATTACTGCAGC	
69GFP5F	AACAGCTATGACATGATTACGAACAAGACGGCGACAAATCC	
69GFP5R	TCTAGCCGGATCCTAACTGCAAAACTCGAGAC	
69GFP3F	GCAGTTAGGATCCGGCTAGAGGAGCAGAGGTTGG	
69GFP3R	GTAAAACGACGGCCAGTGCCAGCAGATGGAGGAGCCATAGC	
69GFPHYGF	GTCTCGAGTTTTGCAGTTAGTGAGCAAGGGCGAGGAGCTG	
69GFPHYGR	AACCTCTGCTCCTCTAGCCGCCTACTGAACGTTATGAC	
Erg11F	TCGAAACCTAATCAATCAACATGGGGTTGCTCTCCGCTGTGC	
Erg11R	GCTCACCATTGCTTTTTTCGGACAGTTGACG	
McherryErg11F	CCGAAAAAGCAATGGTGAGCAAGGGCGAGG	
McherryErg11R	TGCTCATAGTCACATCCCTCACTTGTACAGCTCGTCCATGC	
AP57	TCGAAACCTAATCAATCAACATGGTGAGCAAGGGCGAGG	
AP58	TGCTCATAGTCACATCCCTCAAAGCTTAGACTTGTACAGCTCGTCCATGC	
<b>Primers used for RIP mutation of <i>vdtx</i></b>		
<b>Oligo nucleotide</b>	<b>Sequence</b>	<b>Notes</b>
RIPF1	CCTCTGCAGGTCGACTCTAGACGATGCTAGATCACAAGTCC	Amplification and cloning of 2258 bp of <i>vdtx</i>
RIPR2	GGCCAATTCTTAATTAAGATATCGGCGAGAAATGATGTTTT CC	
RIPseqF	AATTTCCAACGATGCTCAGC	Amplification and sequencing of the native <i>vdtx</i> allele in the region targeted for RIP
RIPseqR	TTGGAACGAATCAGACAAGG	

**Figure S1 UV-vis-spectra and mass spectra for 6, 10, 11, and 12**



**Figure S2. Mutation in *vdtX* via repeat induced point mutation.** The top DNA and predicted amino acid sequences are from wild type and the bottom are from the RIP mutant.

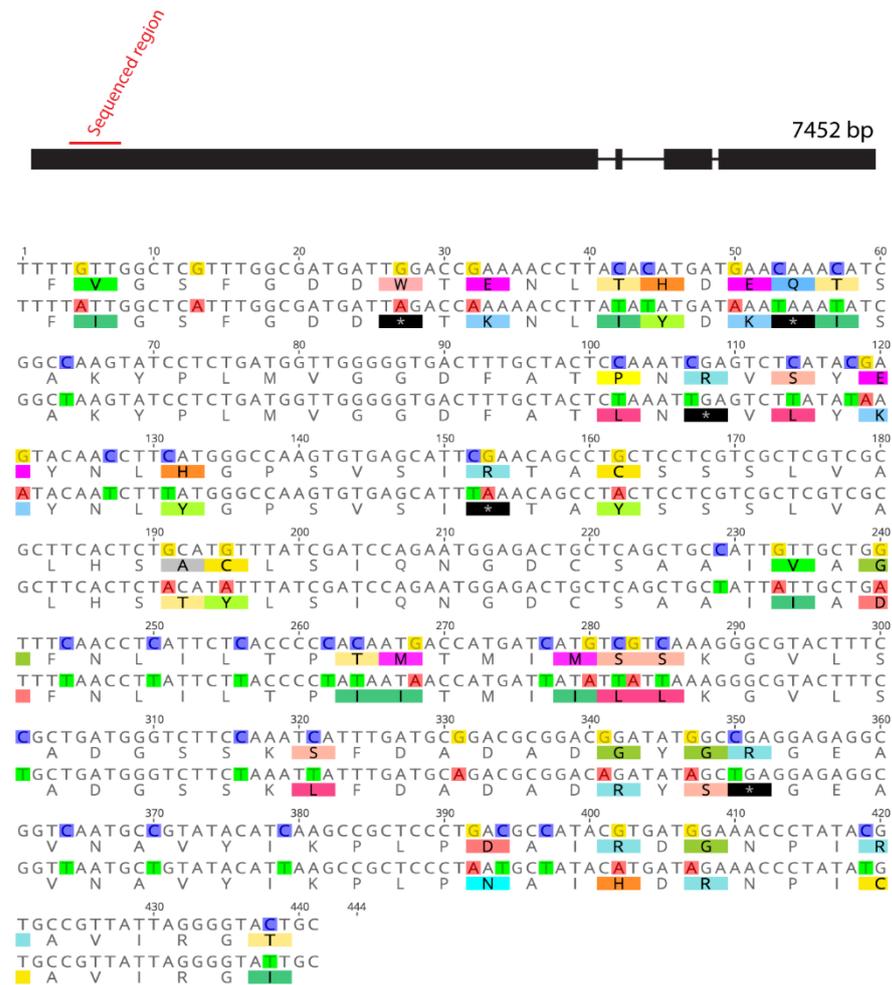


Figure S3. <sup>1</sup>H NMR spectrum (500 MHz) of 1 in chloroform-*d*

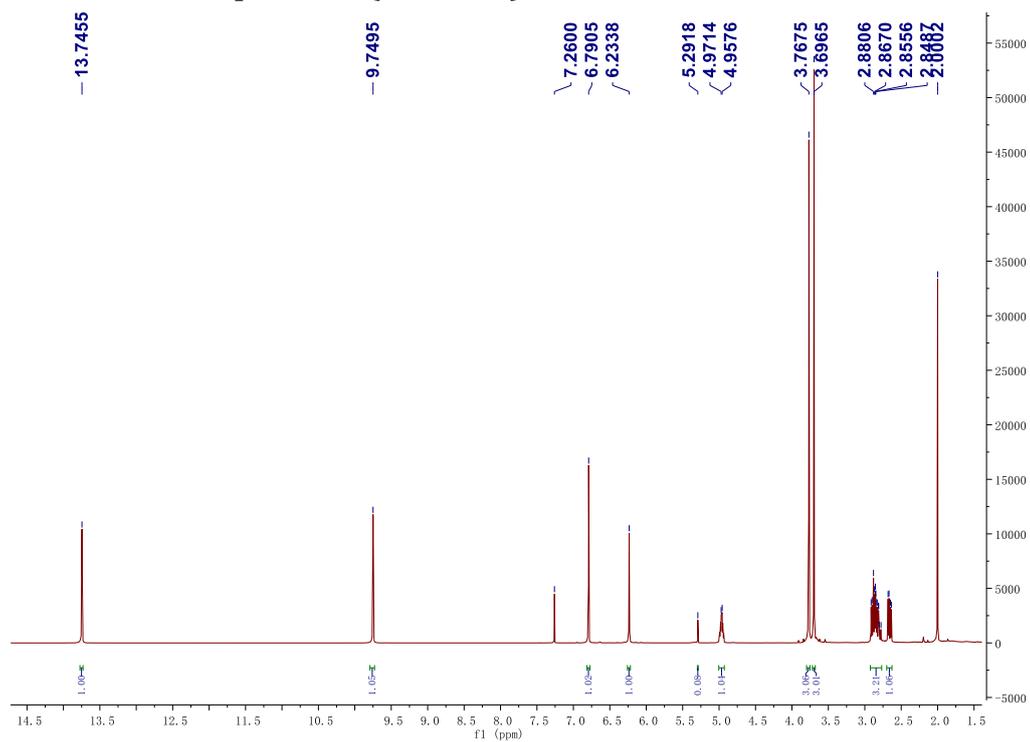
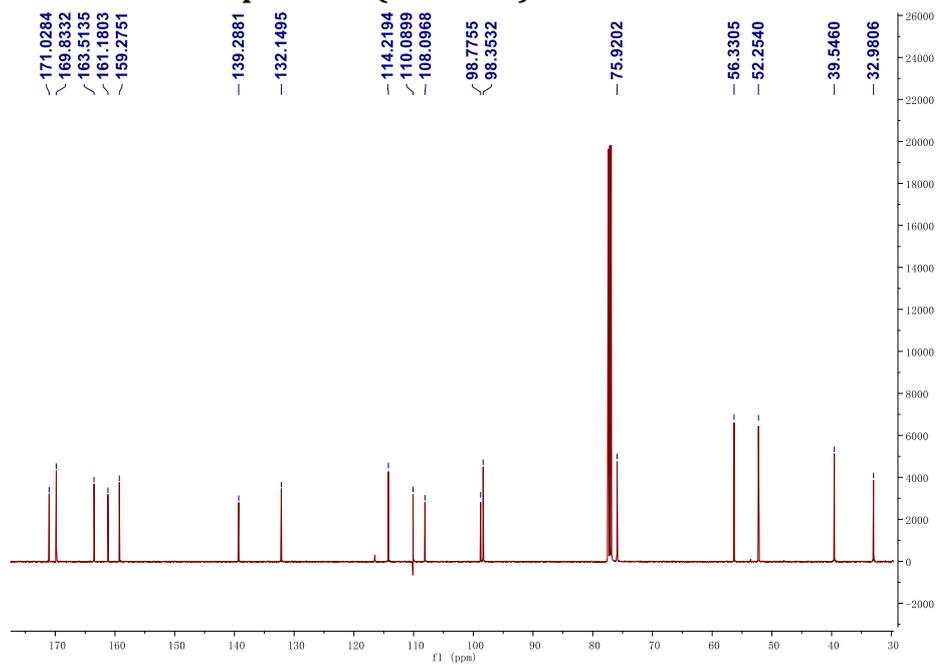
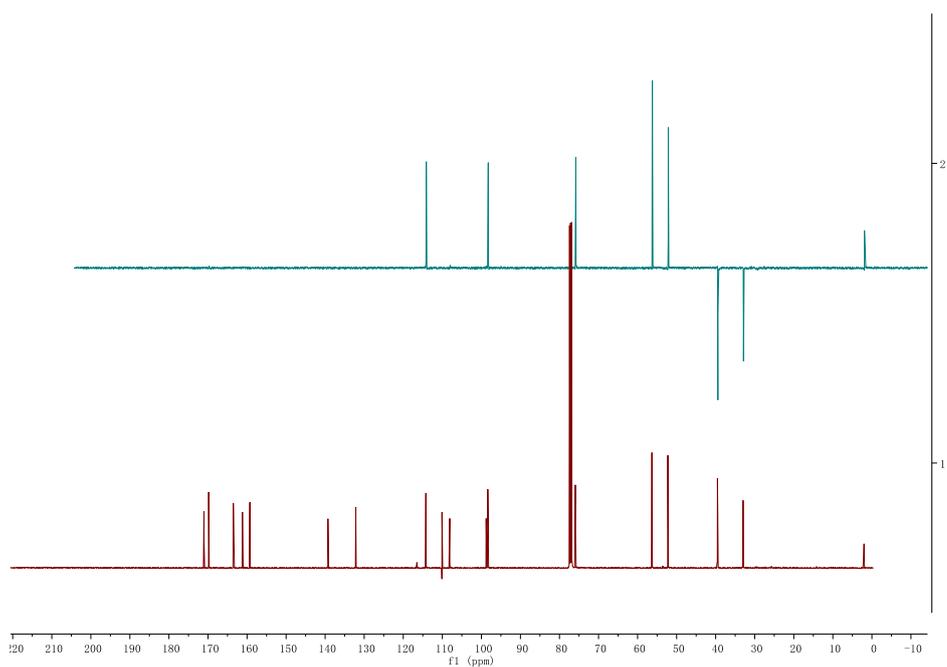


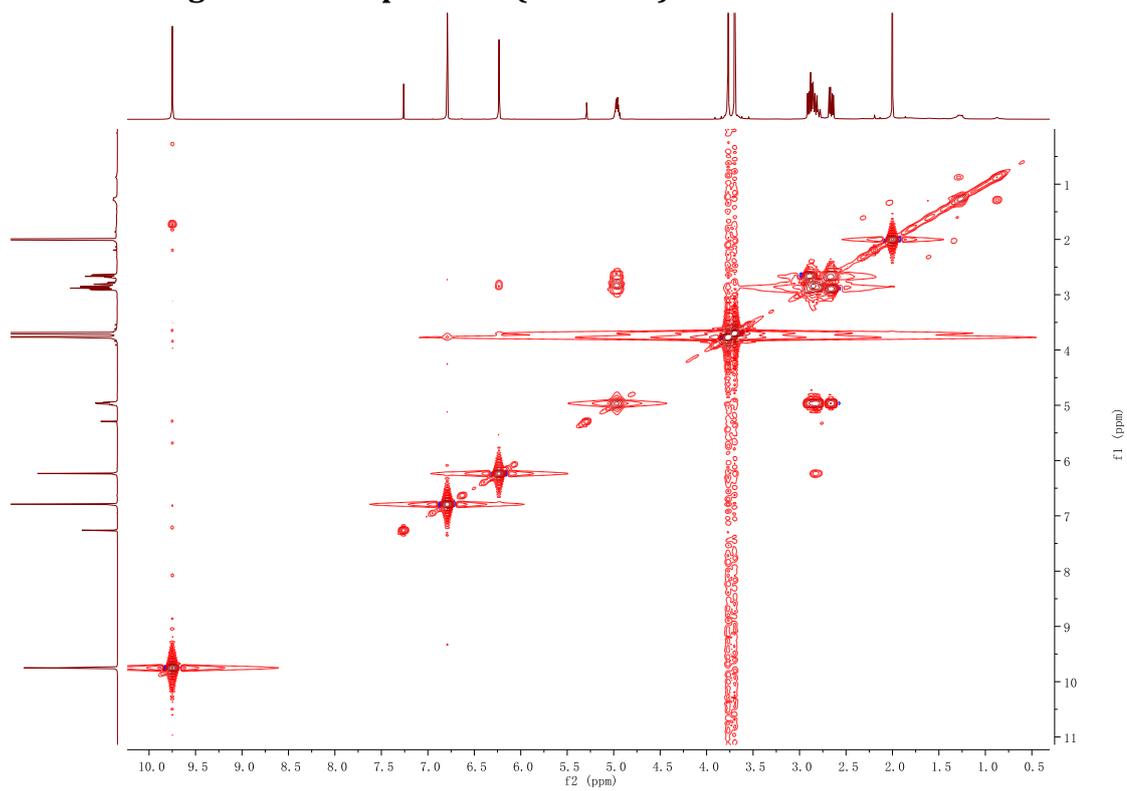
Figure S4.  $^{13}\text{C}$  NMR spectrum (125 MHz) of 1 in chloroform-*d*



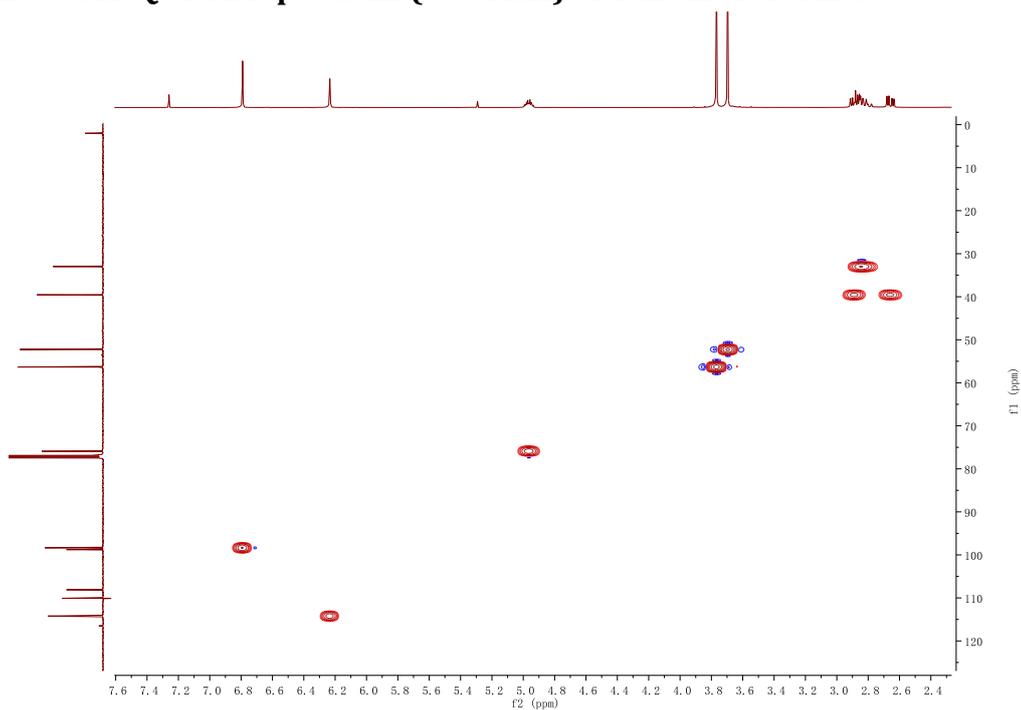
**Figure S5. DEPT-135  $^{13}\text{C}$  NMR spectrum (125 MHz) of 1 in chloroform-*d***



**Figure S6.  $^1\text{H}$ - $^1\text{H}$  gCOSY NMR spectrum (500 MHz) of 1 in chloroform-*d***



**Figure S7. HSQC NMR spectrum (500 MHz) of 1 in chloroform-*d***



**Figure S8. HMBC NMR spectrum (500 MHz) of 1 in chloroform-*d***

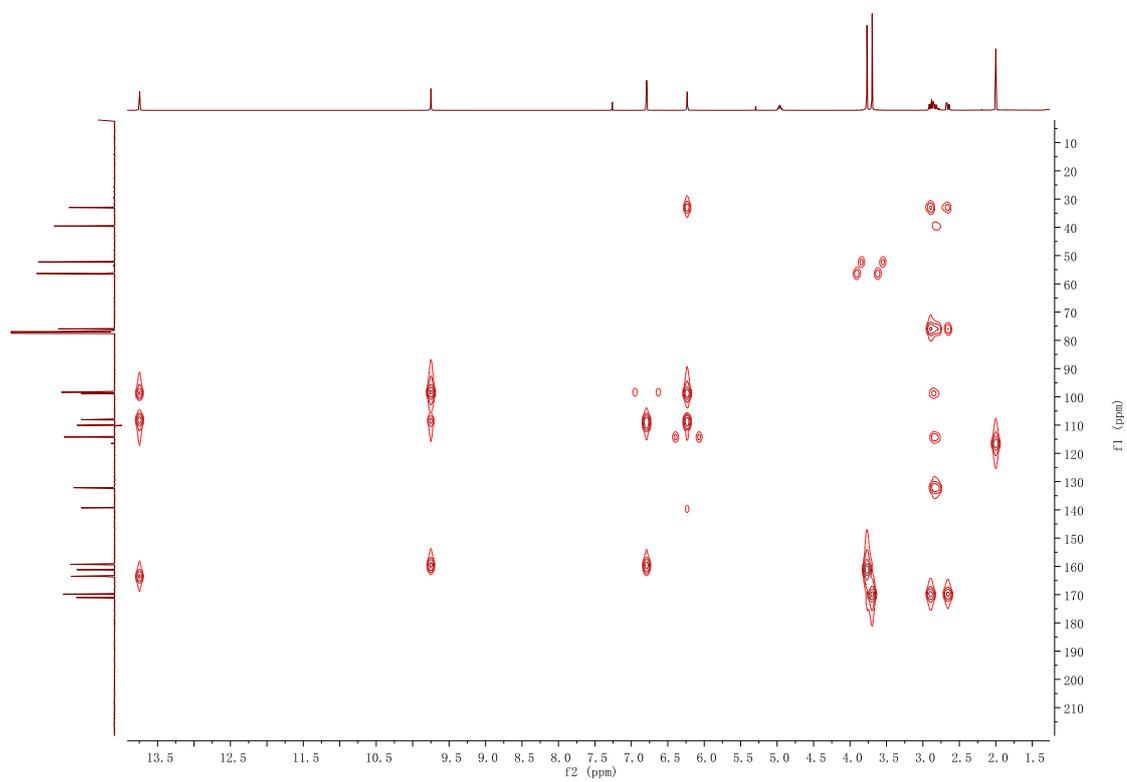


Figure S9. <sup>1</sup>H NMR spectrum (500 MHz) of 1' in chloroform-*d*

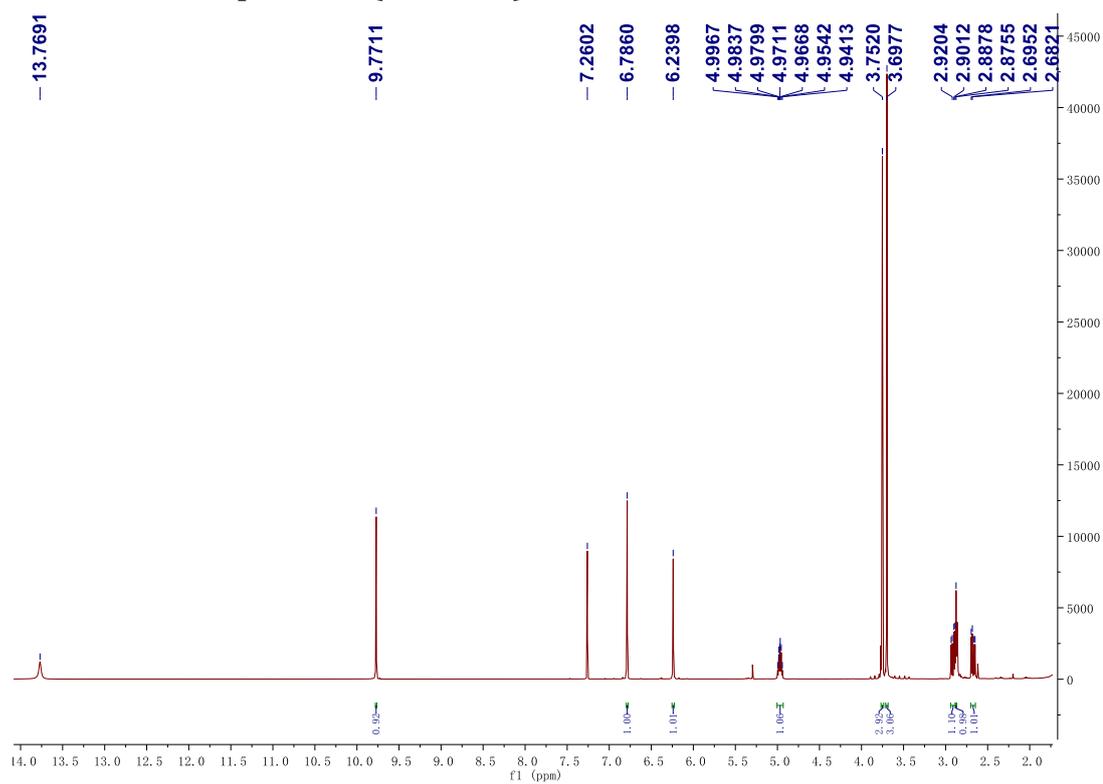
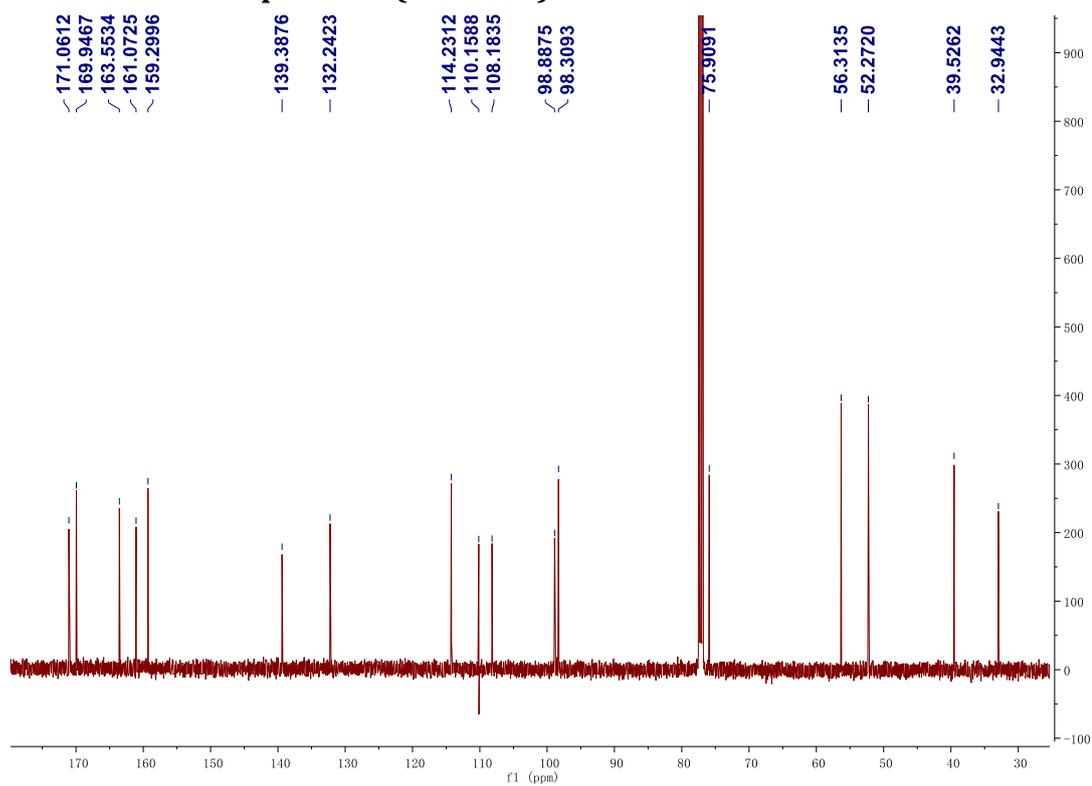
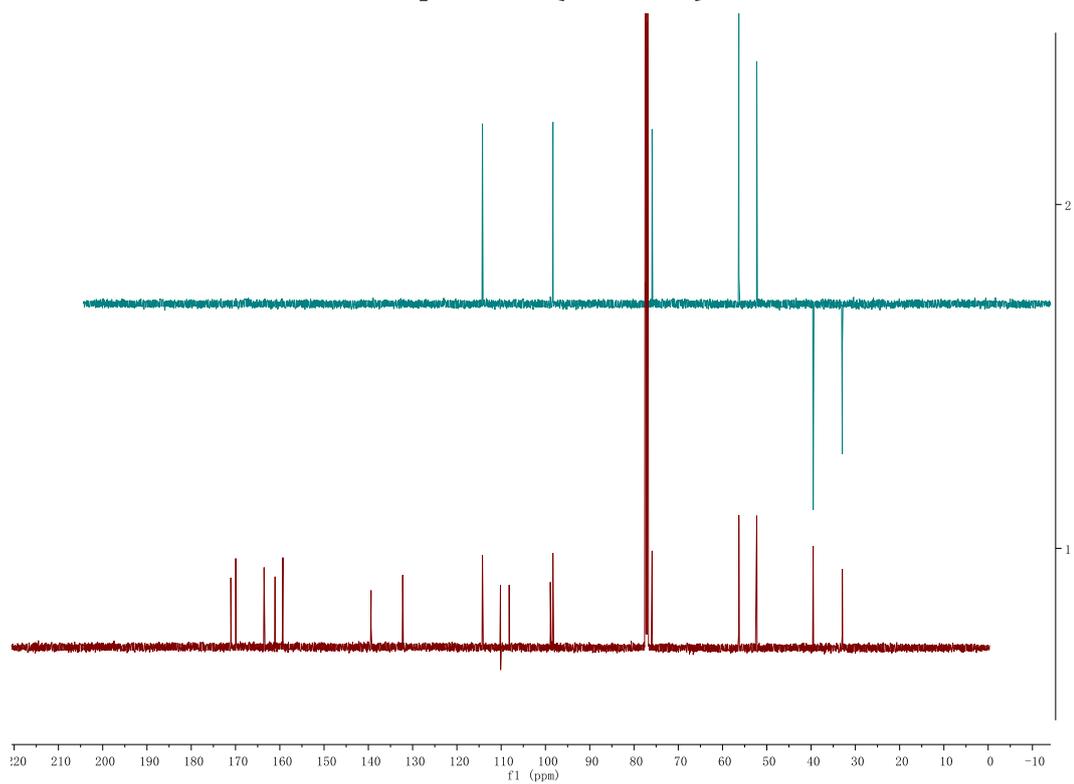


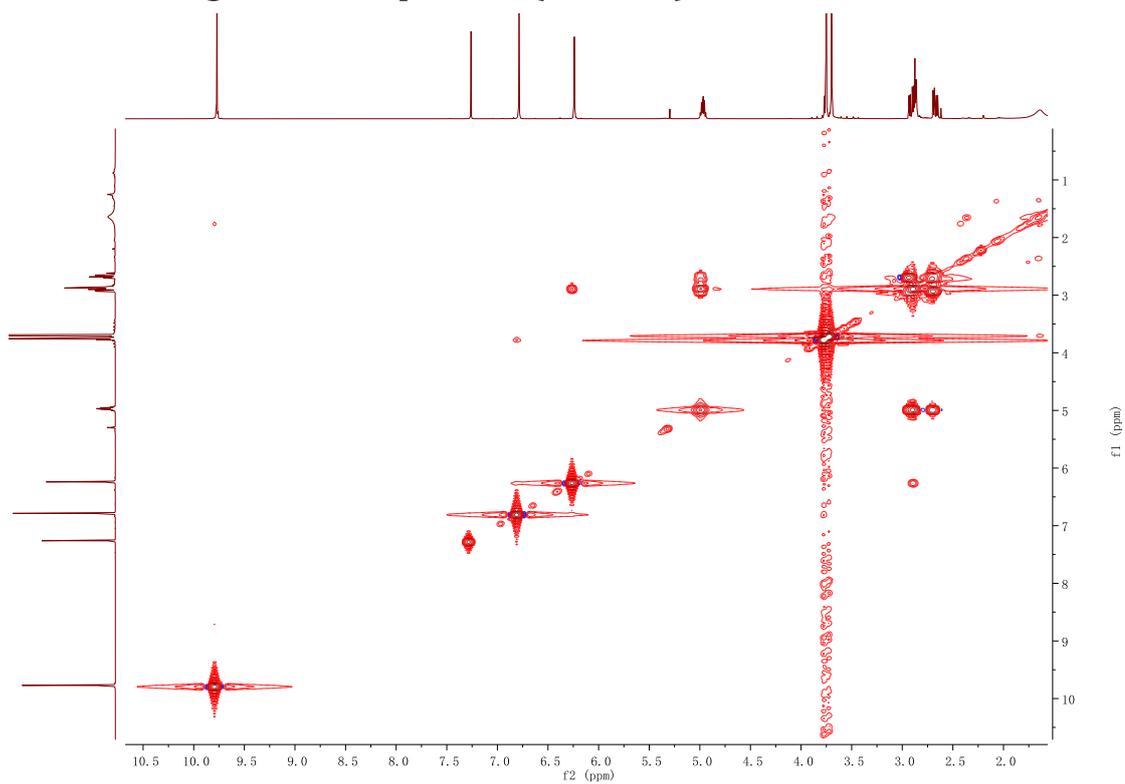
Figure S10.  $^{13}\text{C}$  NMR spectrum (125 MHz) of 1' in chloroform-*d*



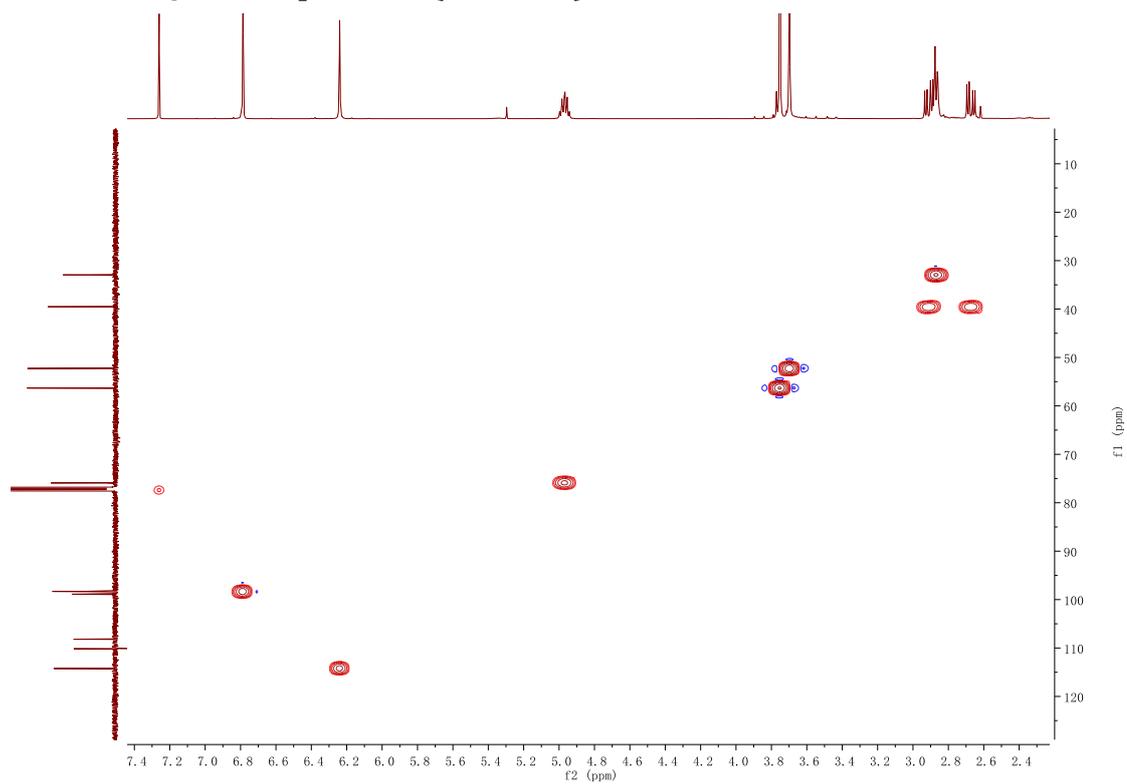
**Figure S11. DEPT-135  $^{13}\text{C}$  NMR spectrum (125 MHz) of 1' in chloroform-*d***



**Figure S12.  $^1\text{H}$ - $^1\text{H}$  gCOSY NMR spectrum (500 MHz) of **1'** in chloroform-*d***



**Figure S13. HSQC NMR spectrum (500 MHz) of 1' in chloroform-*d***



**Figure S14. HMBC NMR spectrum (500 MHz) of 1' in chloroform-*d***

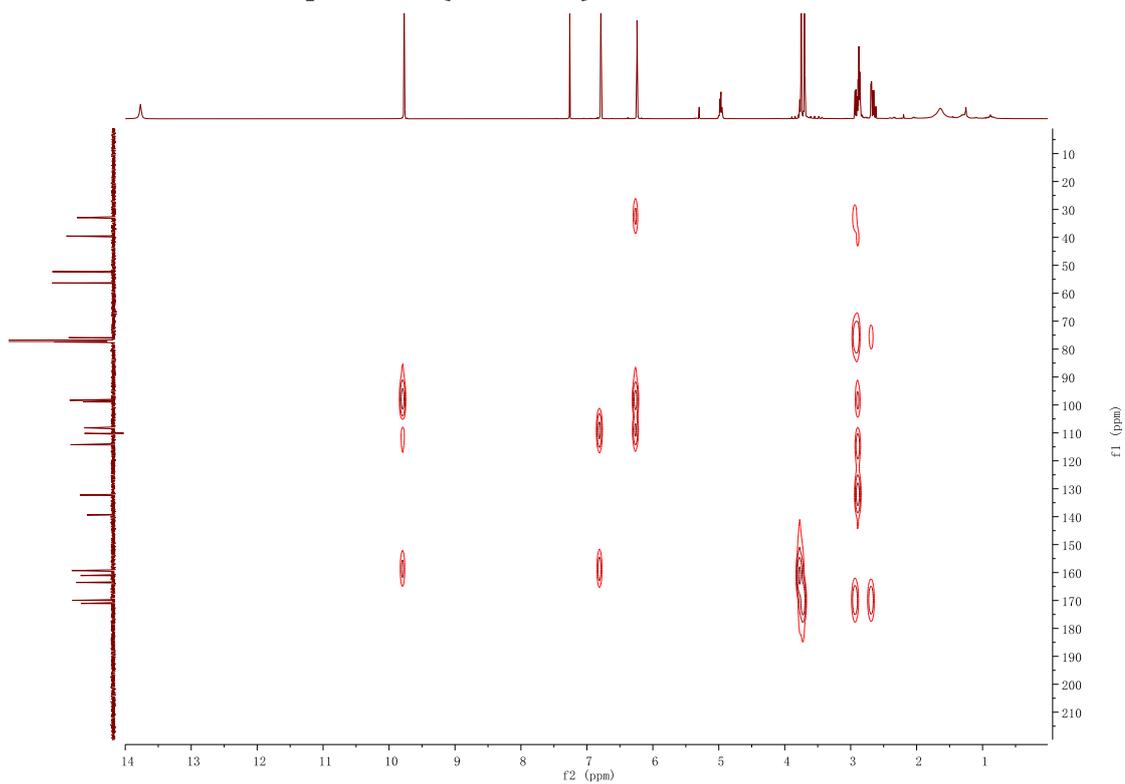


Figure S15.  $^1\text{H}$  NMR spectrum (500 MHz) of 2 in acetonitrile- $d_3$

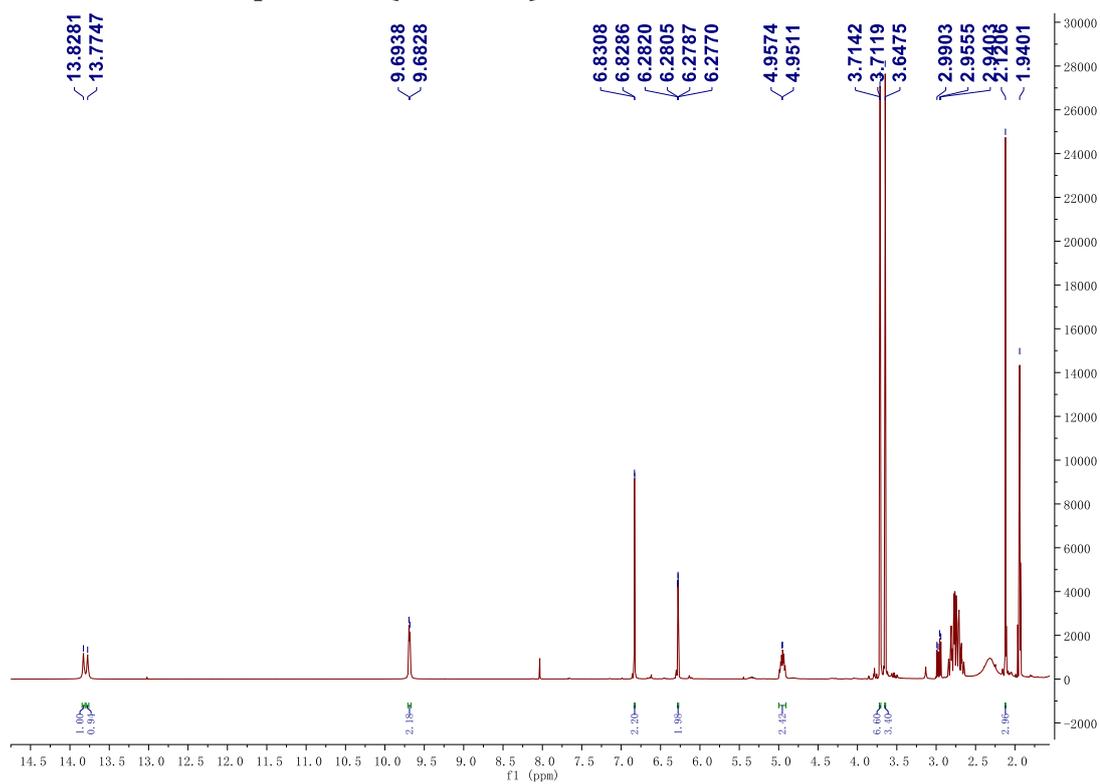
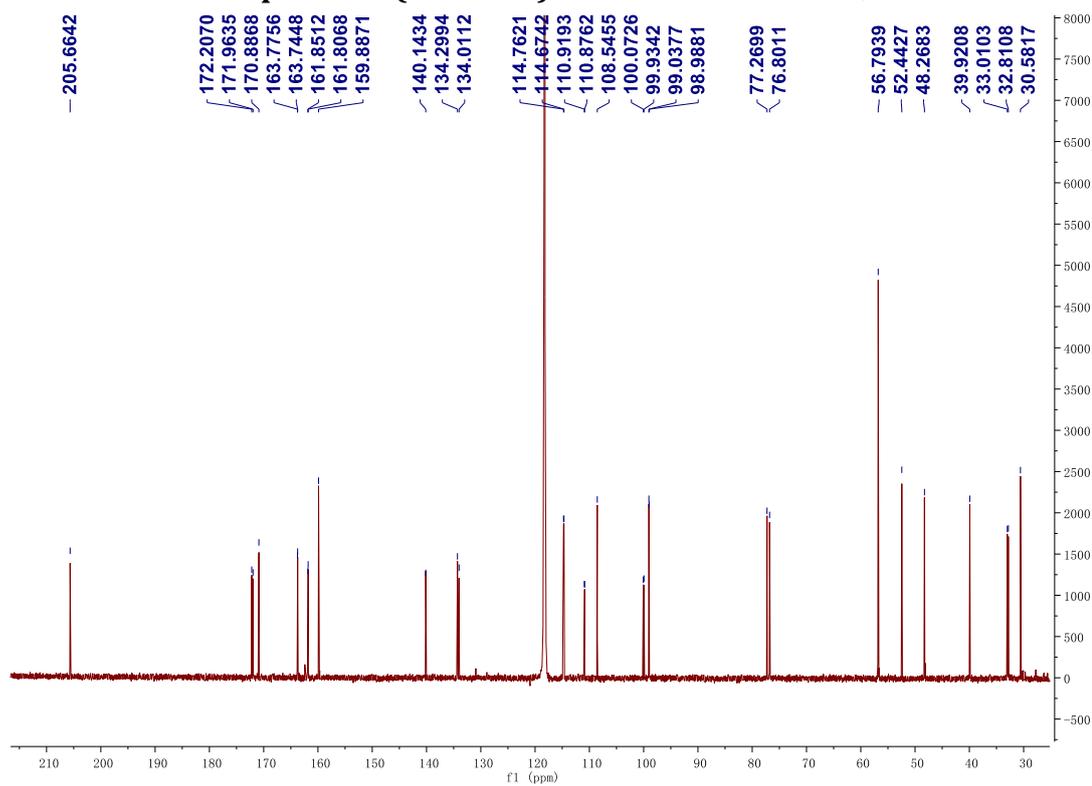
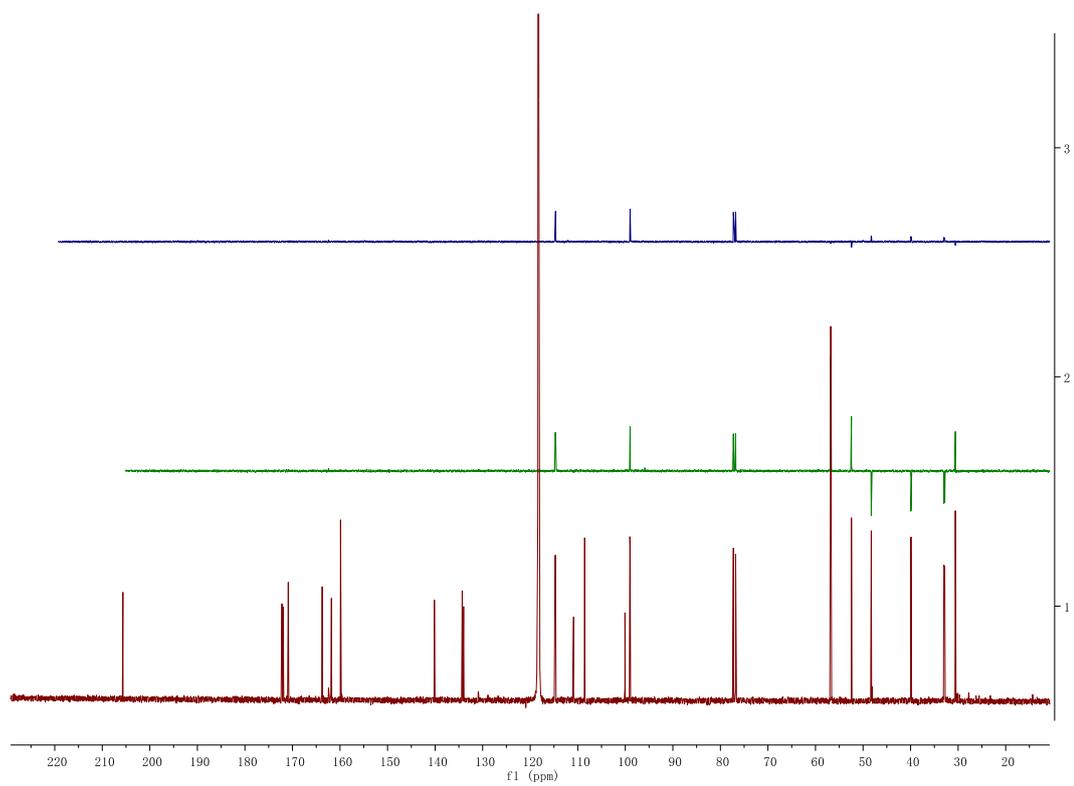


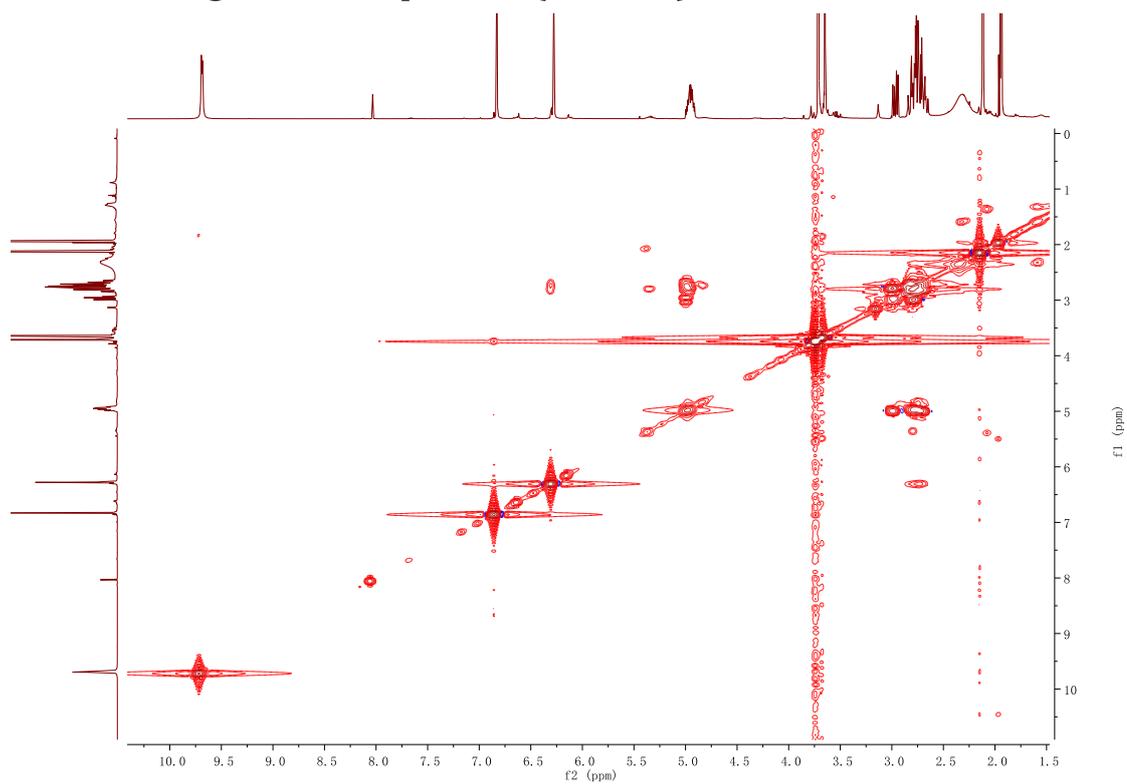
Figure S16.  $^{13}\text{C}$  NMR spectrum (125 MHz) of 2 in acetonitrile- $d_3$



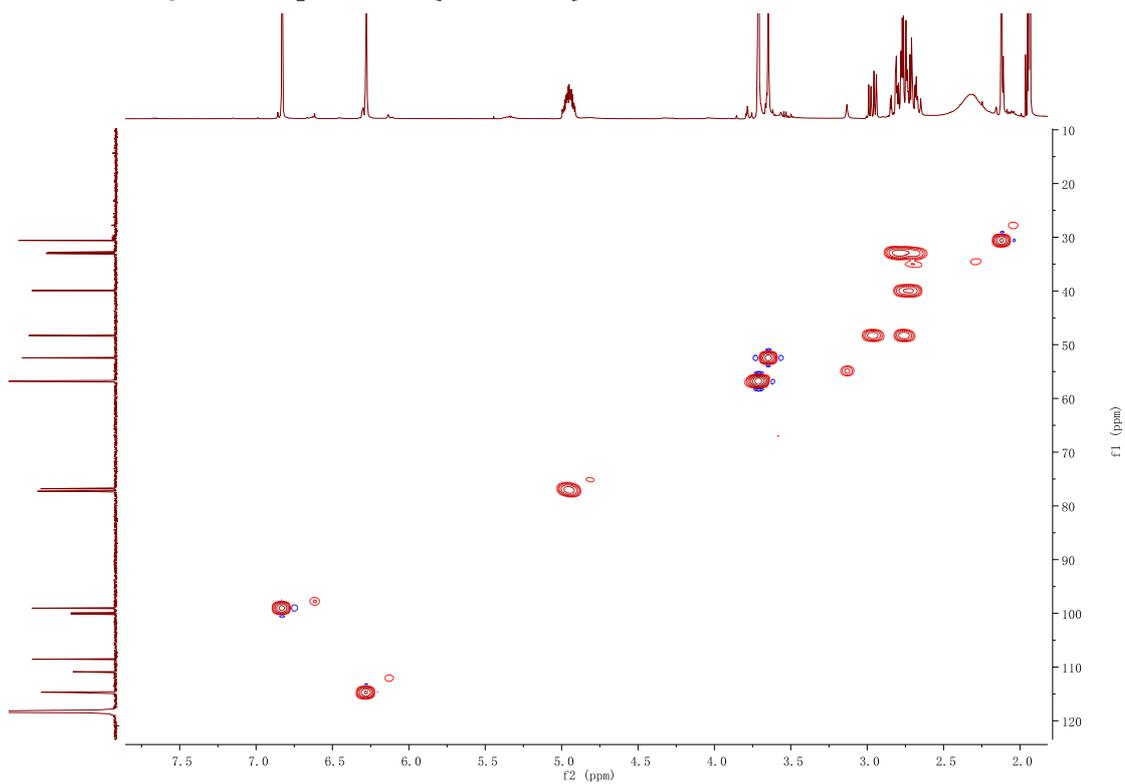
**Figure S17. DEPT-135 and DEPT-90  $^{13}\text{C}$  NMR spectrum (125 MHz) of 2 in acetonitrile- $d_3$**



**Figure S18.  $^1\text{H}$ - $^1\text{H}$  gCOSY NMR spectrum (500 MHz) of 2 in acetonitrile- $d_3$**



**Figure S19. HSQC NMR spectrum (500 MHz) of 2 in acetonitrile- $d_3$**



**Figure S20. HMBC NMR spectrum (500 MHz) of 2 in acetonitrile- $d_3$**

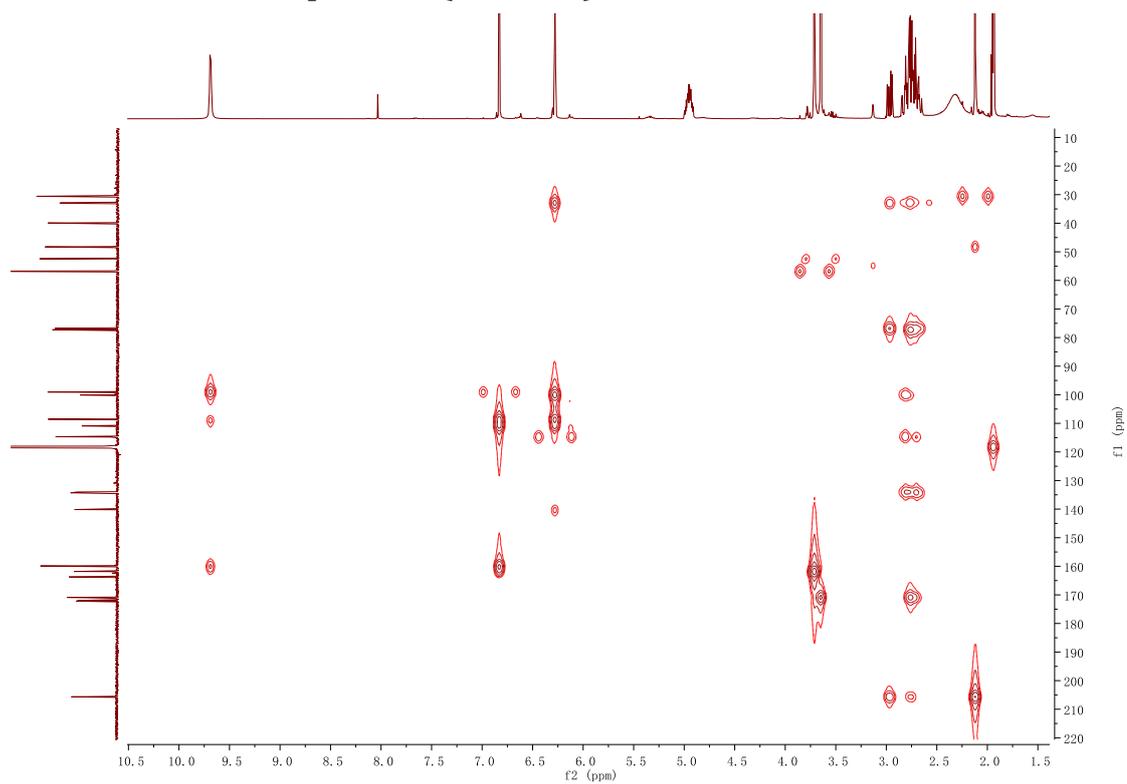


Figure S21.  $^1\text{H}$  NMR spectrum (600 MHz) of 3 in acetonitrile- $d_3$

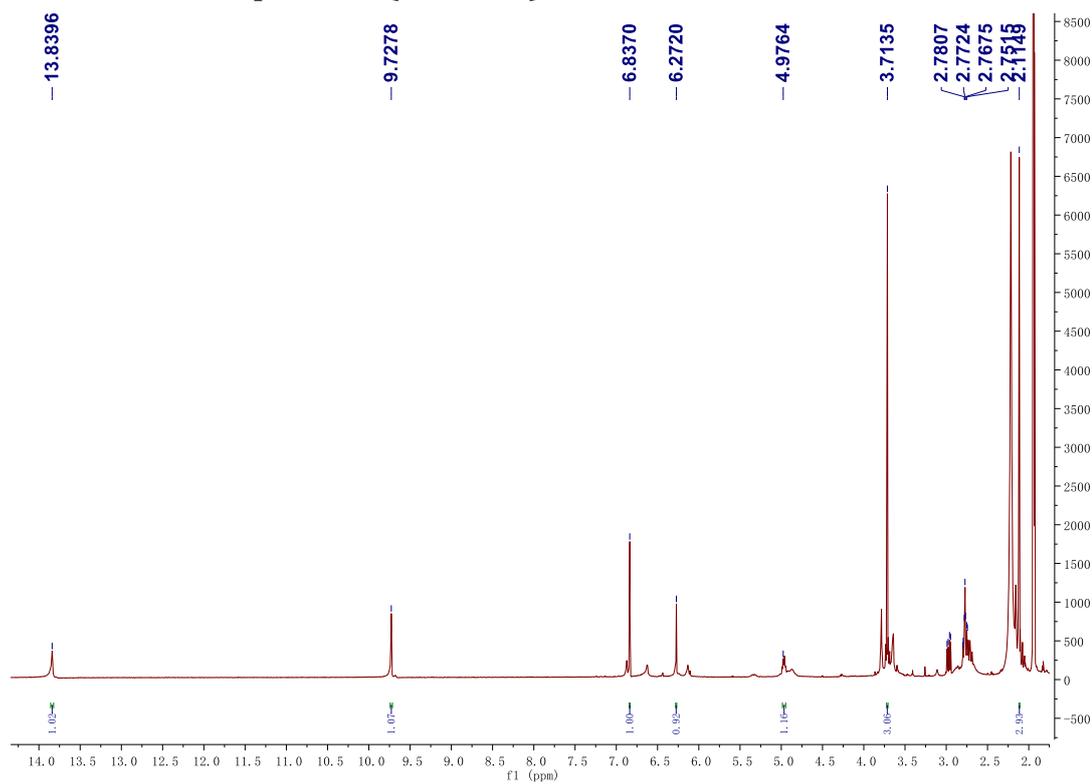


Figure S22.  $^{13}\text{C}$  NMR spectrum (150 MHz) of 3 in acetonitrile- $d_3$

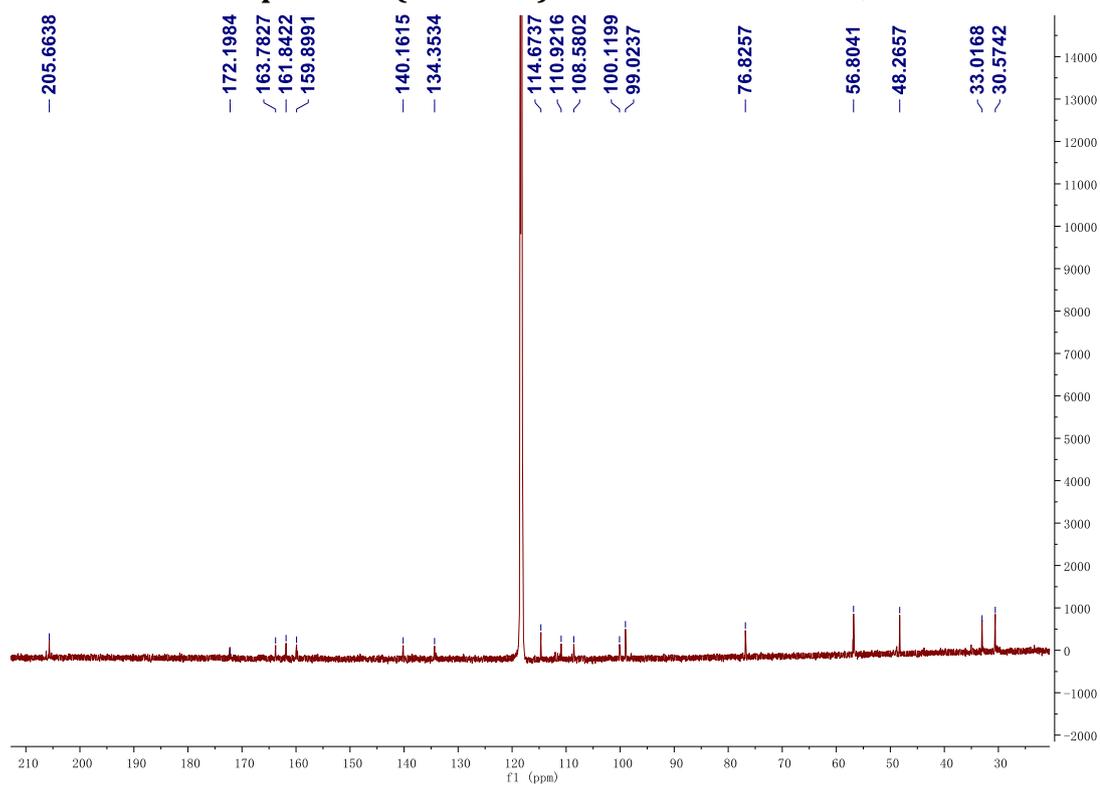
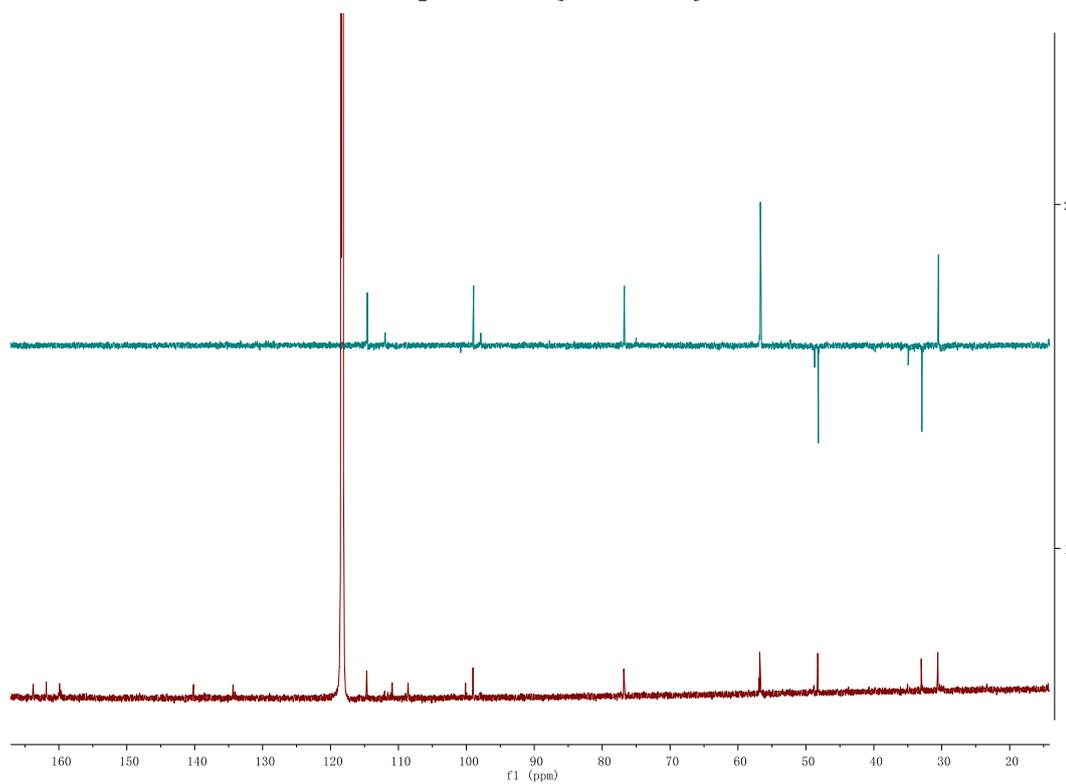


Figure S23. DEPT-135  $^{13}\text{C}$  NMR spectrum (150 MHz) of 3 in acetonitrile- $d_3$



**Figure S24.  $^1\text{H}$ - $^1\text{H}$  gCOSY NMR spectrum (600 MHz) of 3 in acetonitrile- $d_3$**

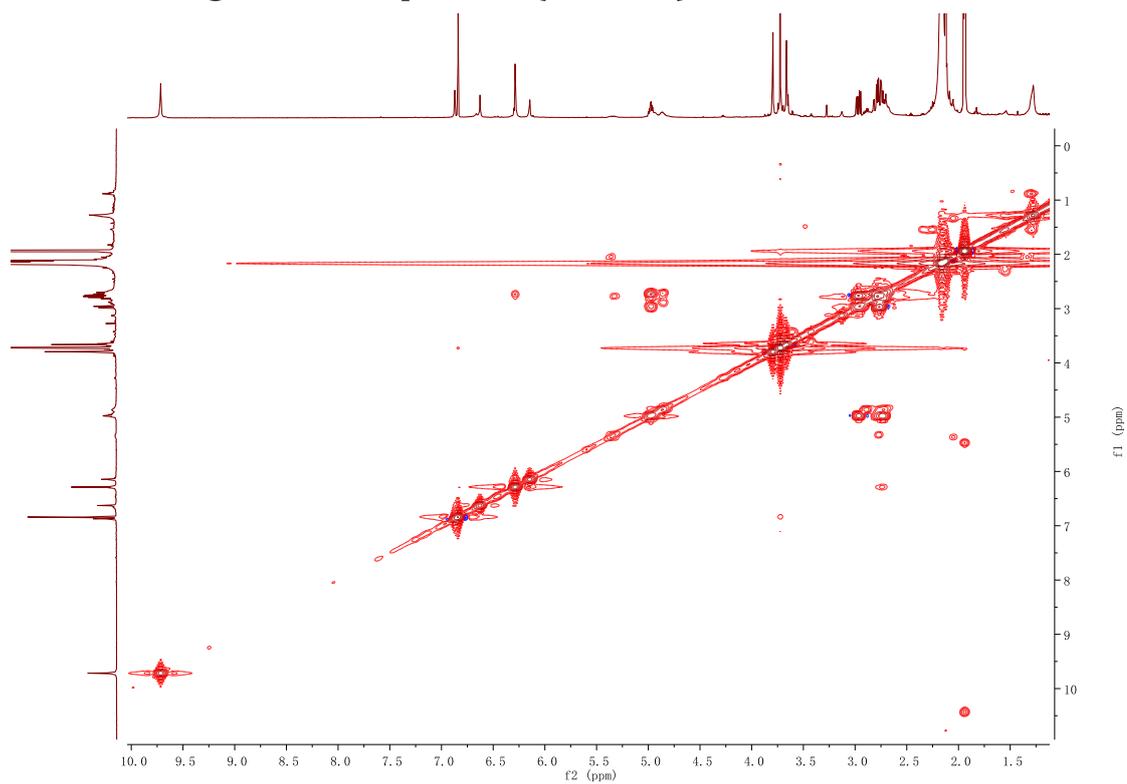


Figure S25. HSQC NMR spectrum (600 MHz) of 3 in acetonitrile- $d_3$

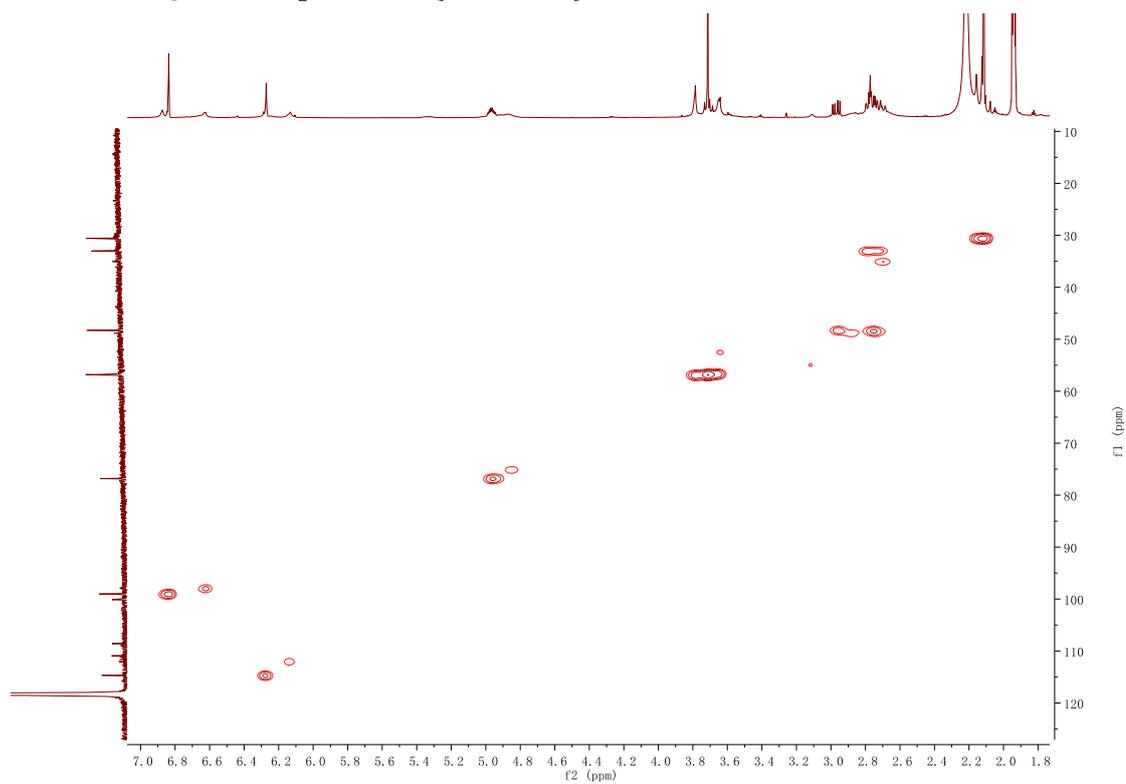


Figure S26. HMBC NMR spectrum (600 MHz) of 3 in acetonitrile- $d_3$

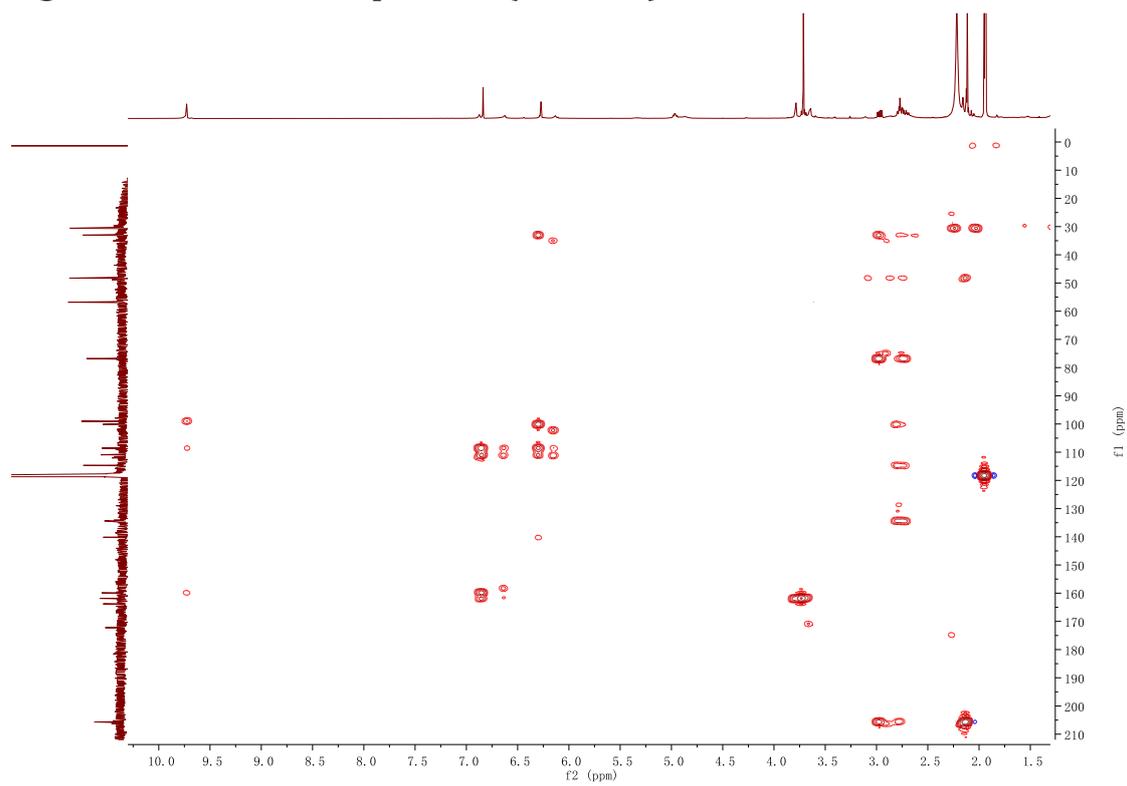


Figure S27.  $^1\text{H}$  NMR spectrum (500 MHz) of 4 in acetonitrile- $d_3$

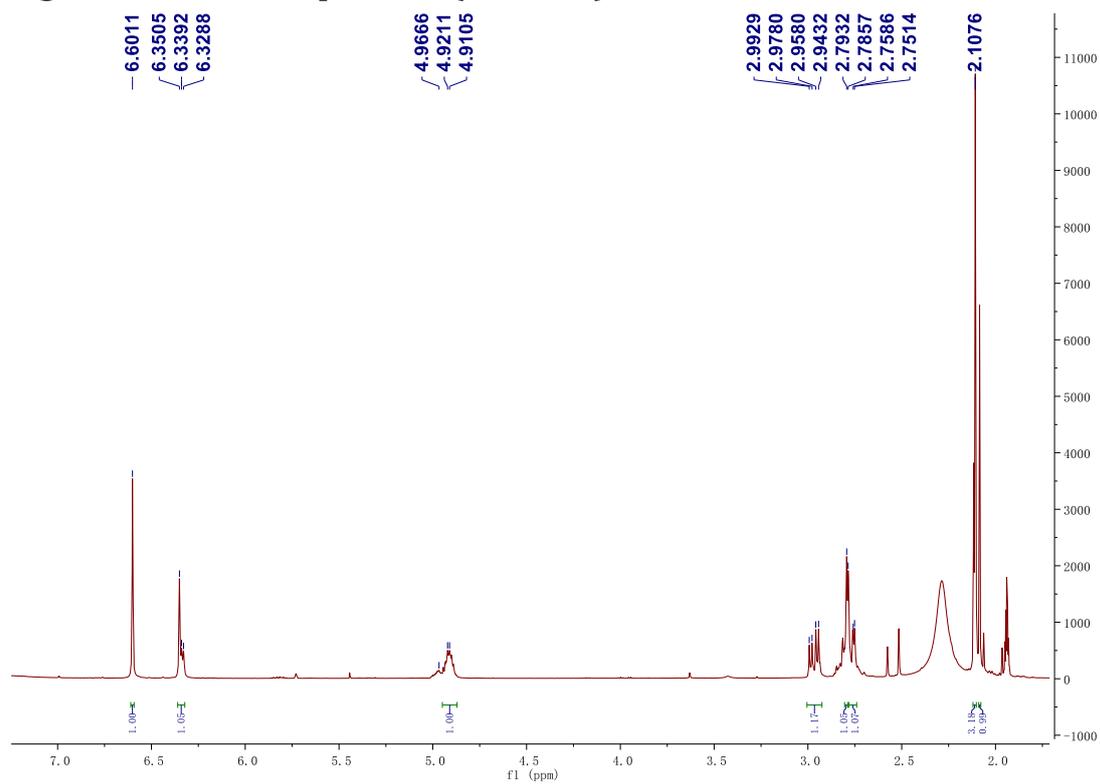


Figure S28.  $^{13}\text{C}$  NMR spectrum (125 MHz) of 4 in acetonitrile- $d_3$

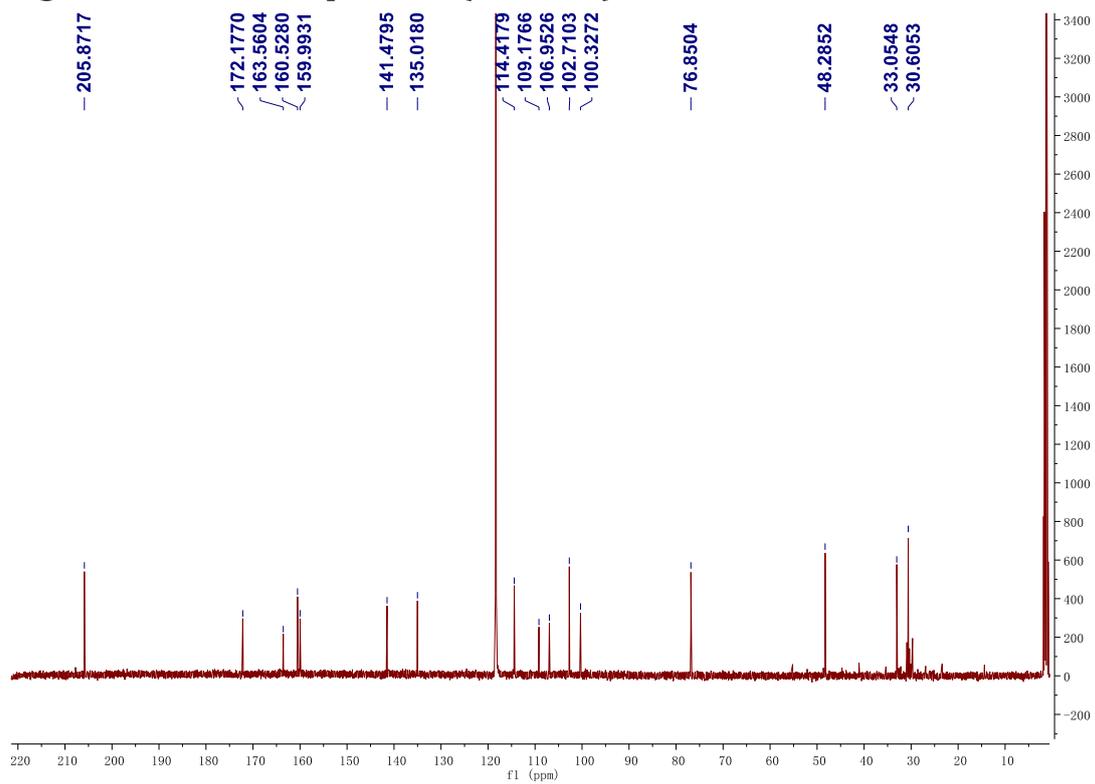
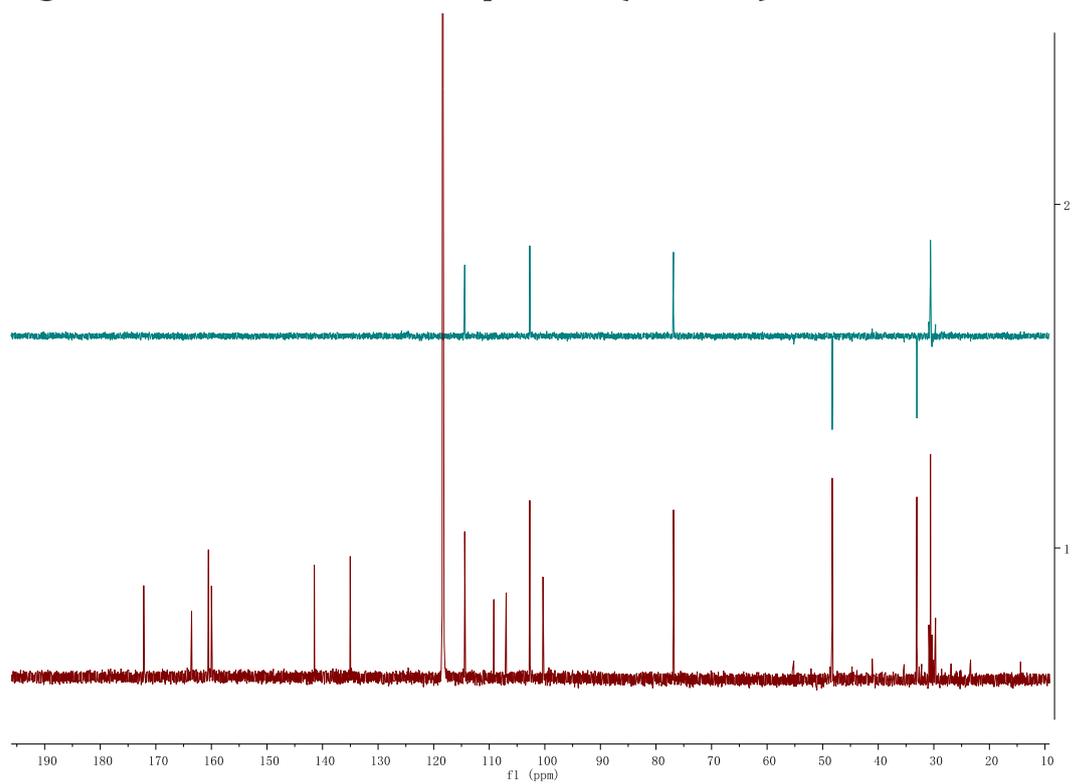


Figure S29. DEPT-135  $^{13}\text{C}$  NMR spectrum (125 MHz) of 4 in acetonitrile- $d_3$



**Figure S30.  $^1\text{H}$ - $^1\text{H}$  gCOSY NMR spectrum (500 MHz) of 4 in acetonitrile- $d_3$**

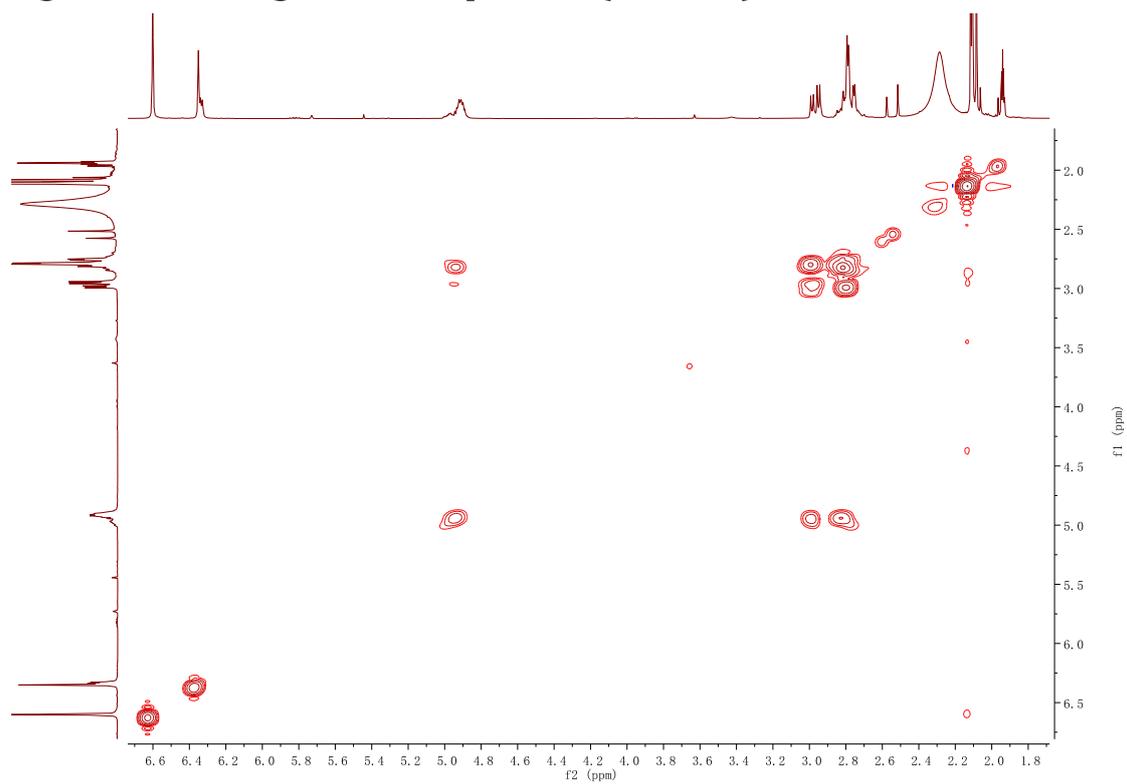
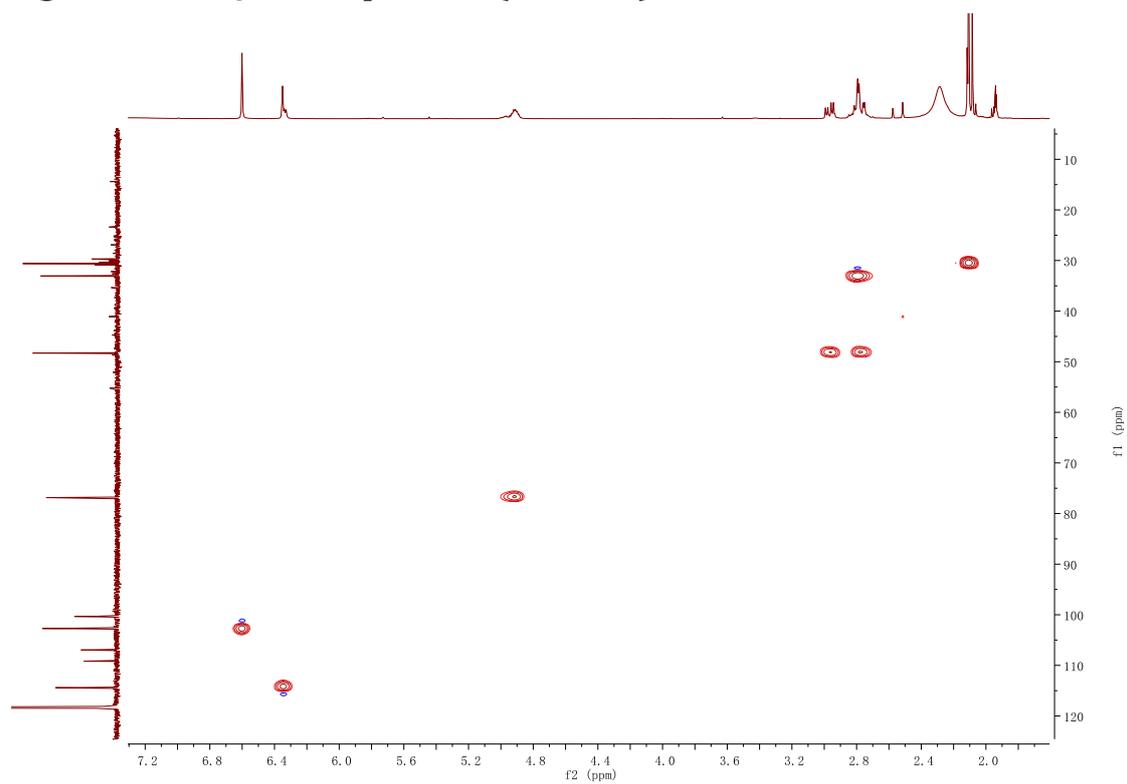


Figure S31. HSQC NMR spectrum (500 MHz) of 4 in acetonitrile- $d_3$



**Figure S32. HMBC NMR spectrum (500 MHz) of 4 in acetonitrile- $d_3$**

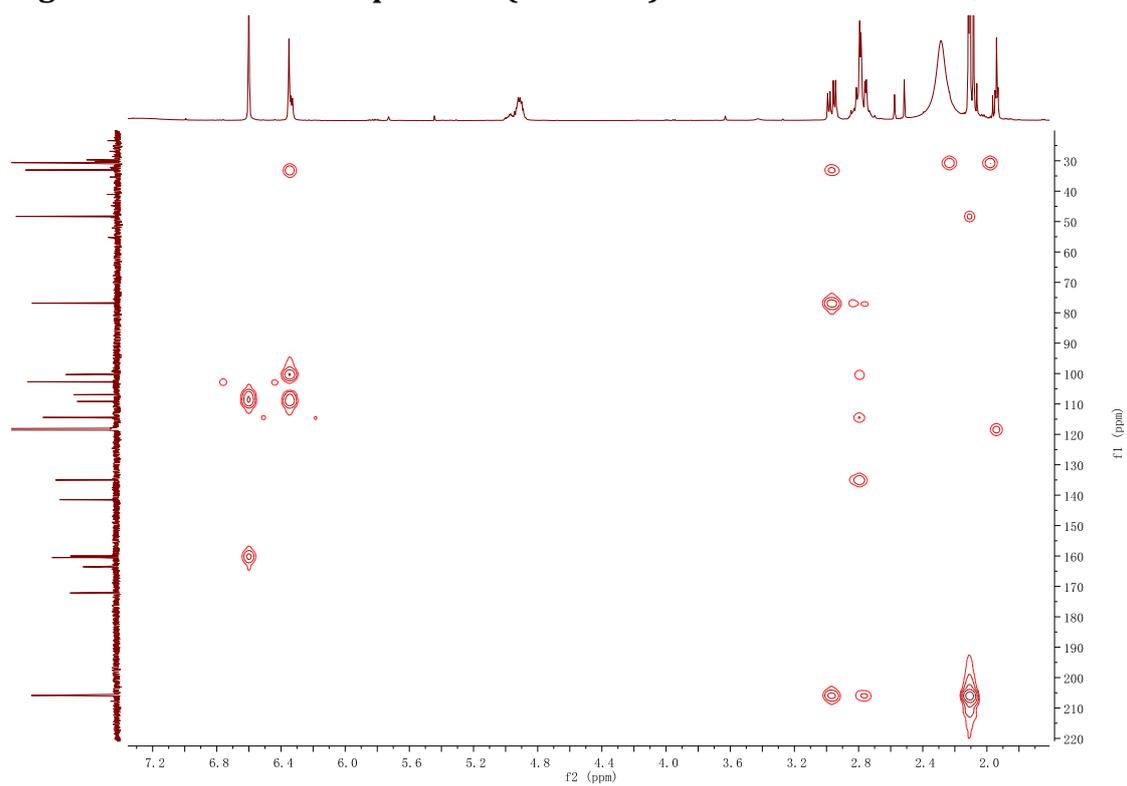


Figure S33.  $^1\text{H}$  NMR spectrum (600 MHz) of 5 in acetonitrile- $d_3$

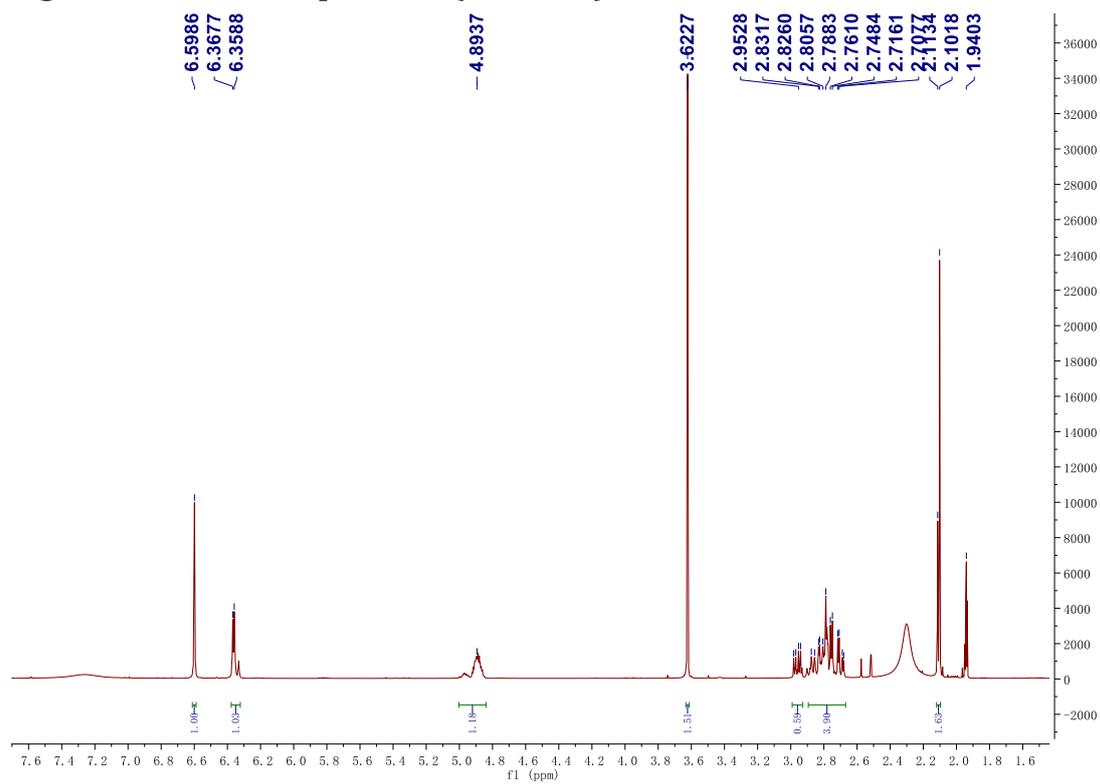
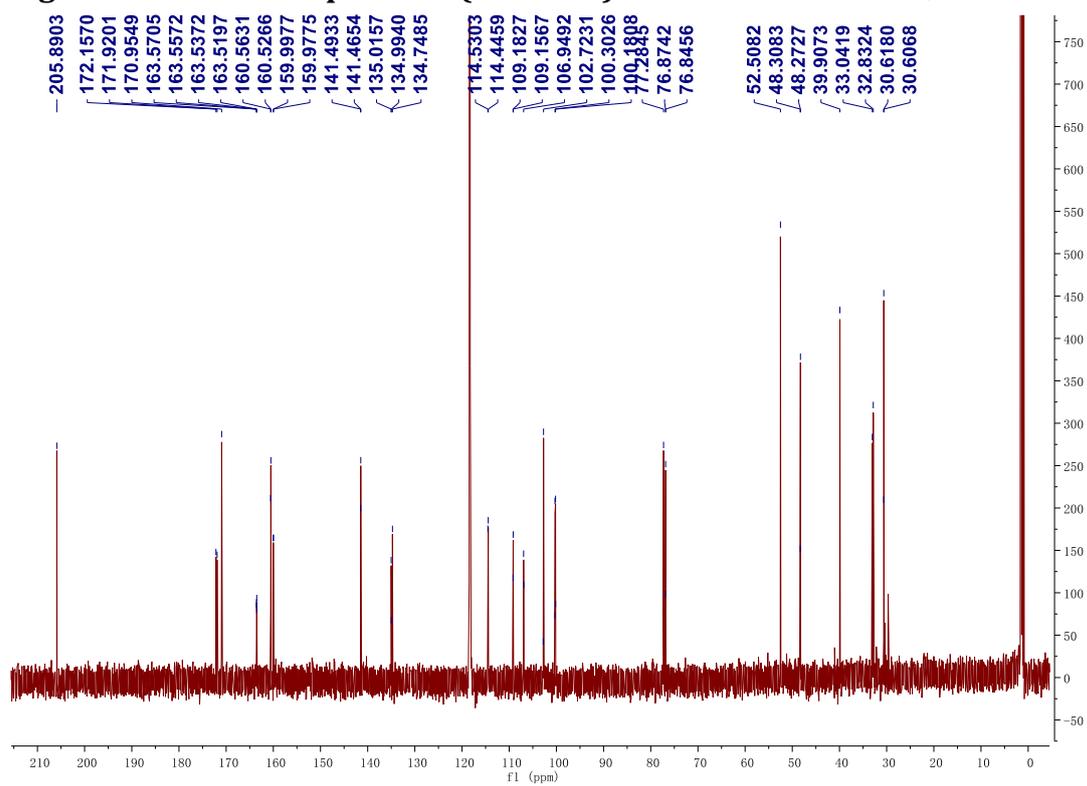
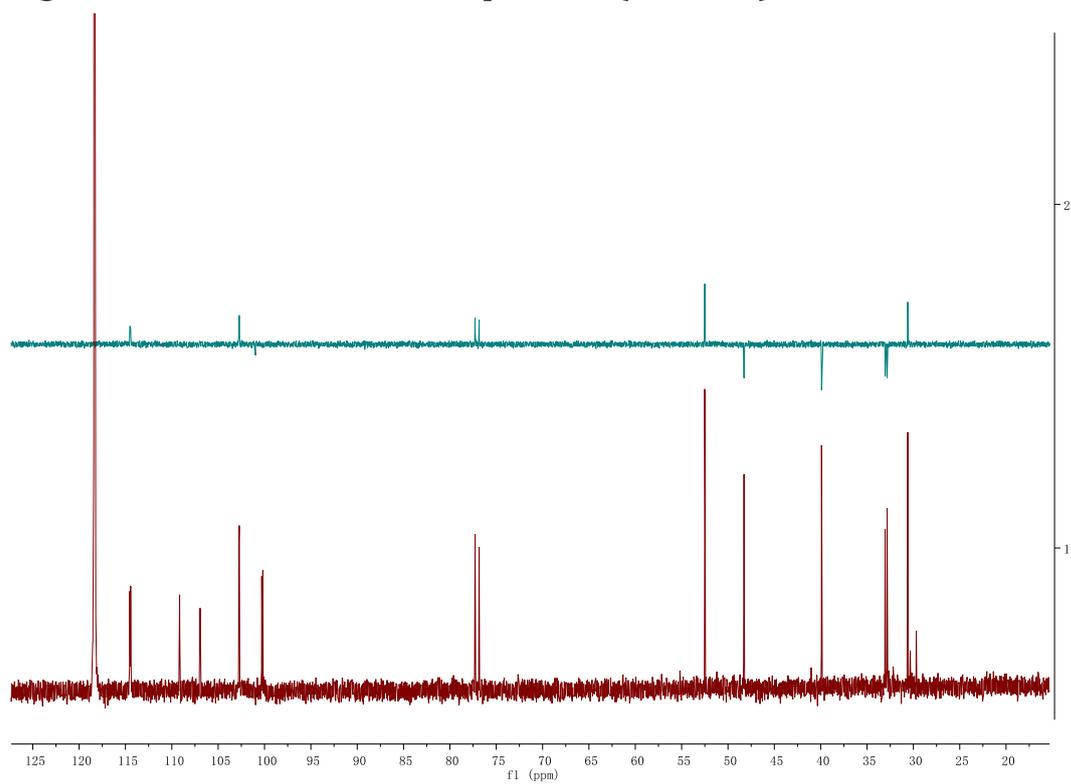


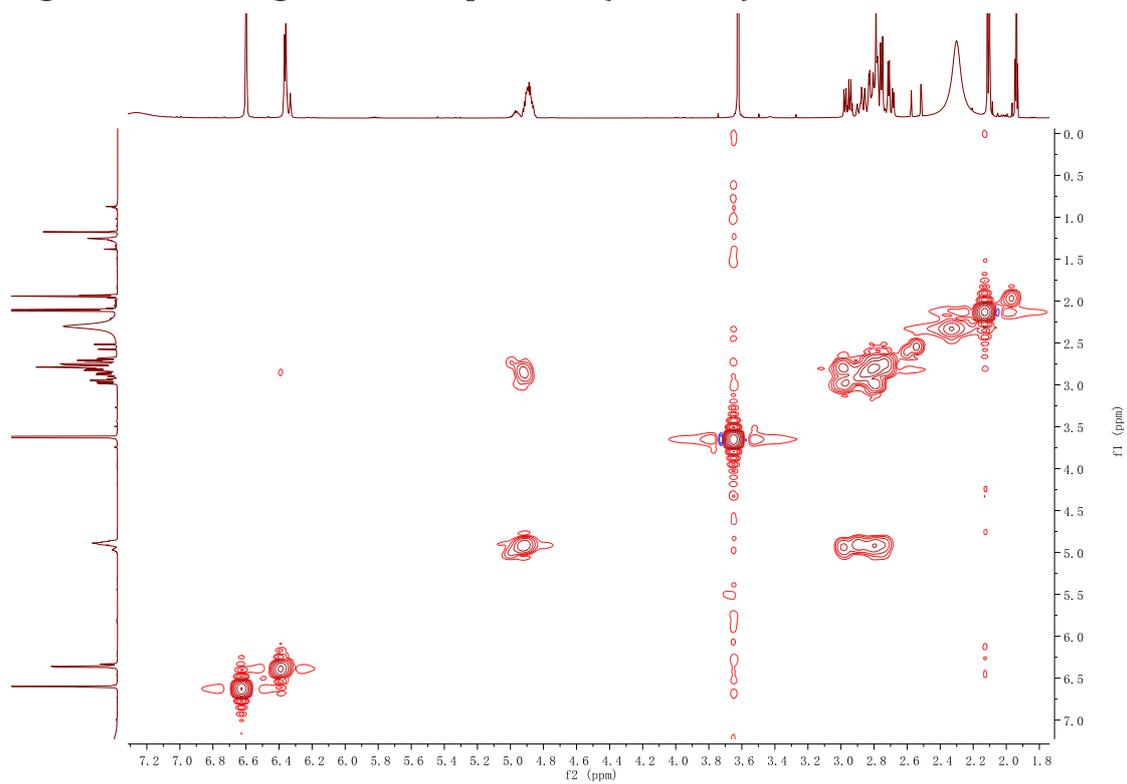
Figure S34. <sup>13</sup>C NMR spectrum (150 MHz) of 5 in acetonitrile-*d*<sub>3</sub>



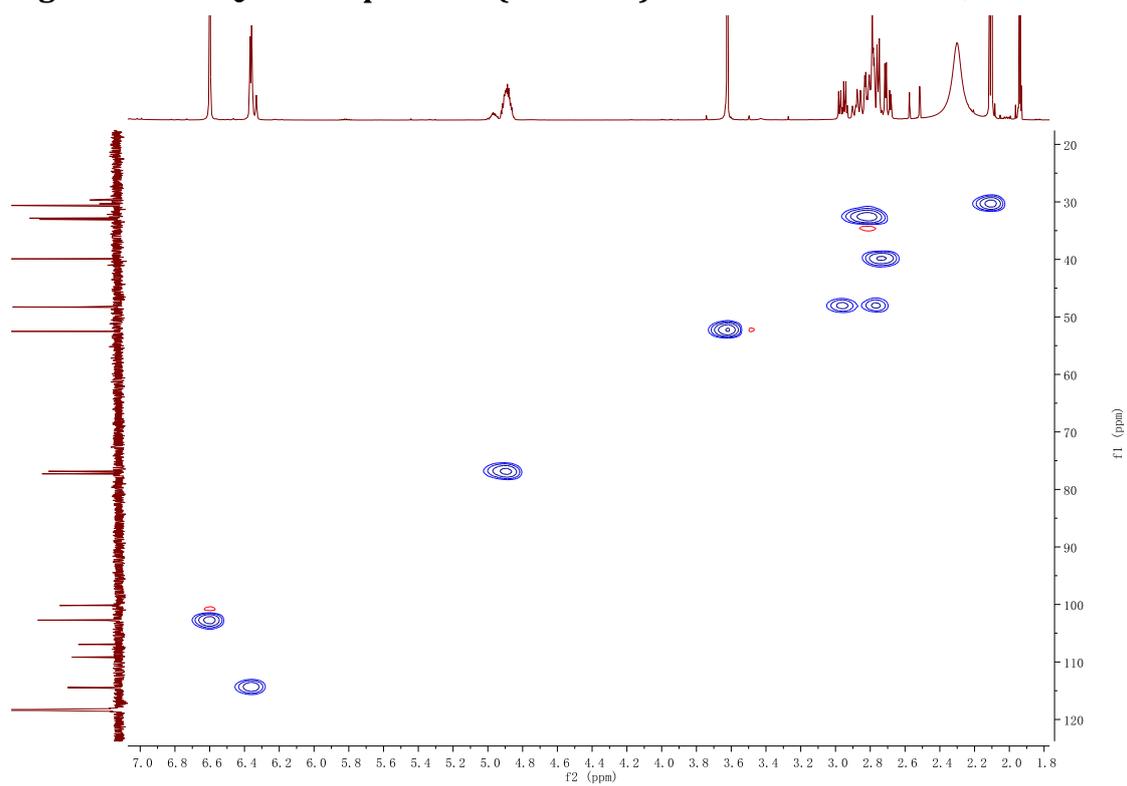
**Figure S35. DEPT-135  $^{13}\text{C}$  NMR spectrum (150 MHz) of 5 in acetonitrile- $d_3$**



**Figure S36.  $^1\text{H}$ - $^1\text{H}$  gCOSY NMR spectrum (500 MHz) of **5** in acetonitrile- $d_3$**



**Figure S37. HSQC NMR spectrum (600 MHz) of 5 in acetonitrile- $d_3$**



**Figure S38. HMBC NMR spectrum (600 MHz) of 5 in acetonitrile- $d_3$**

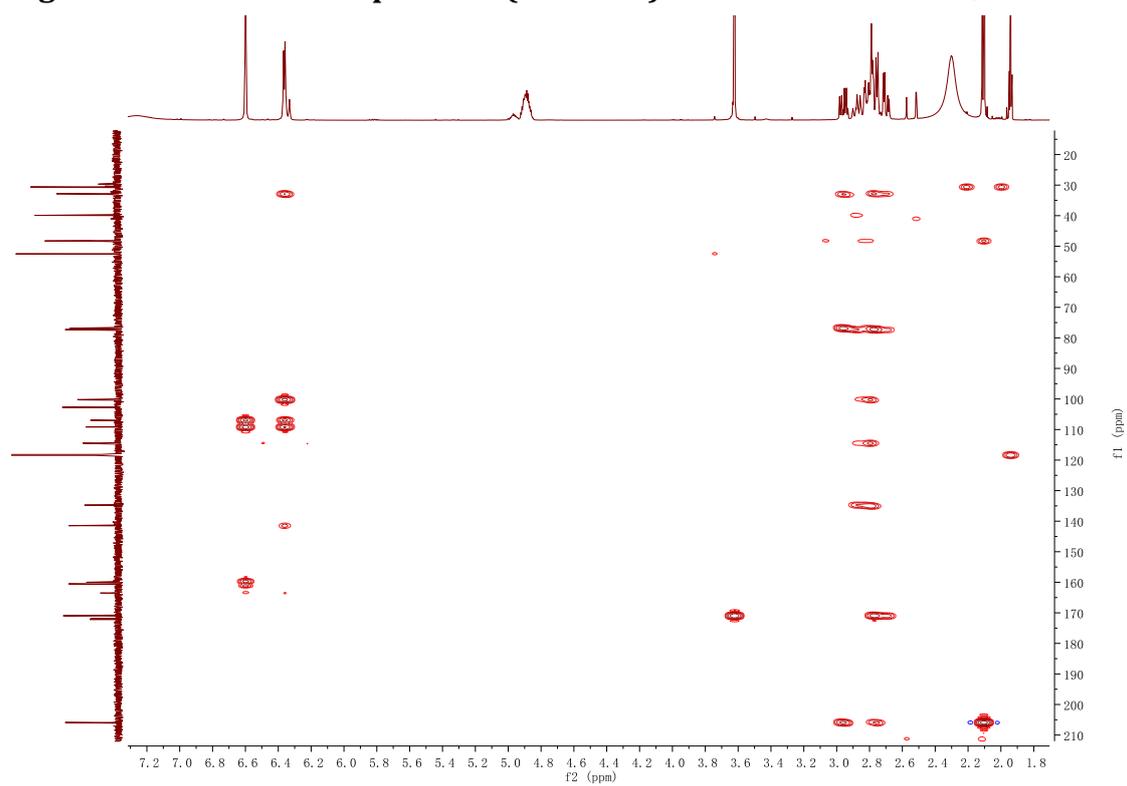


Figure S39.  $^1\text{H}$  NMR spectrum (500 MHz) of 7 in chloroform- $d$

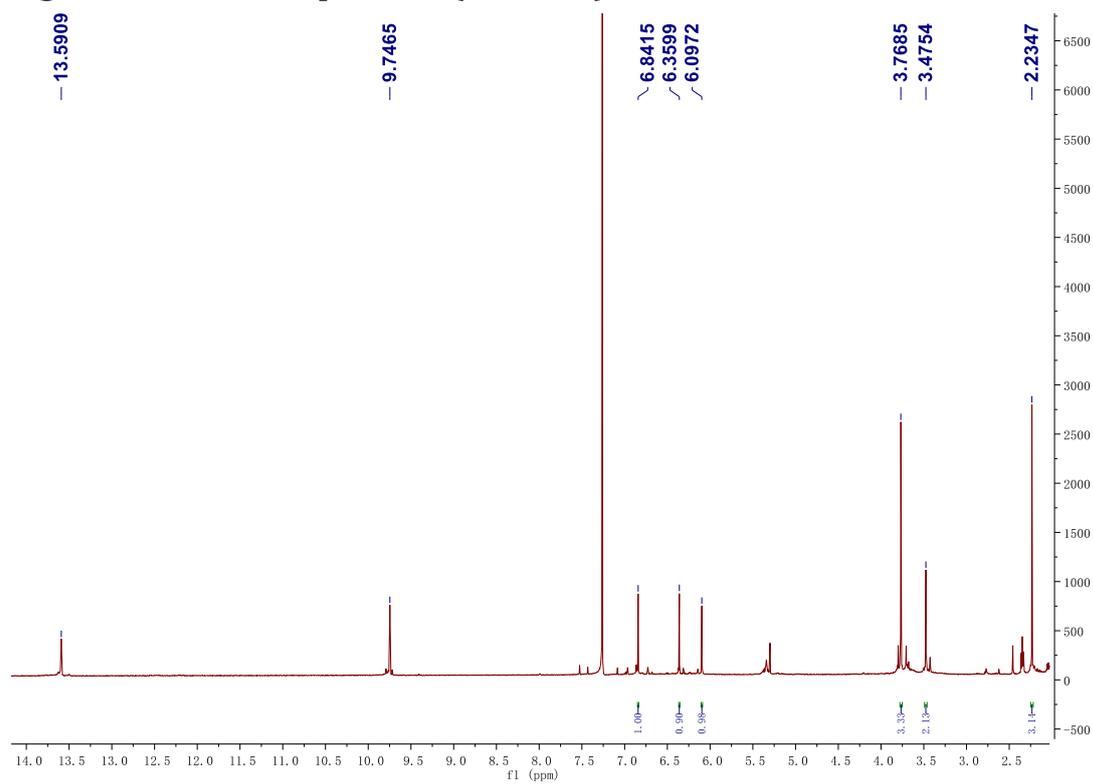
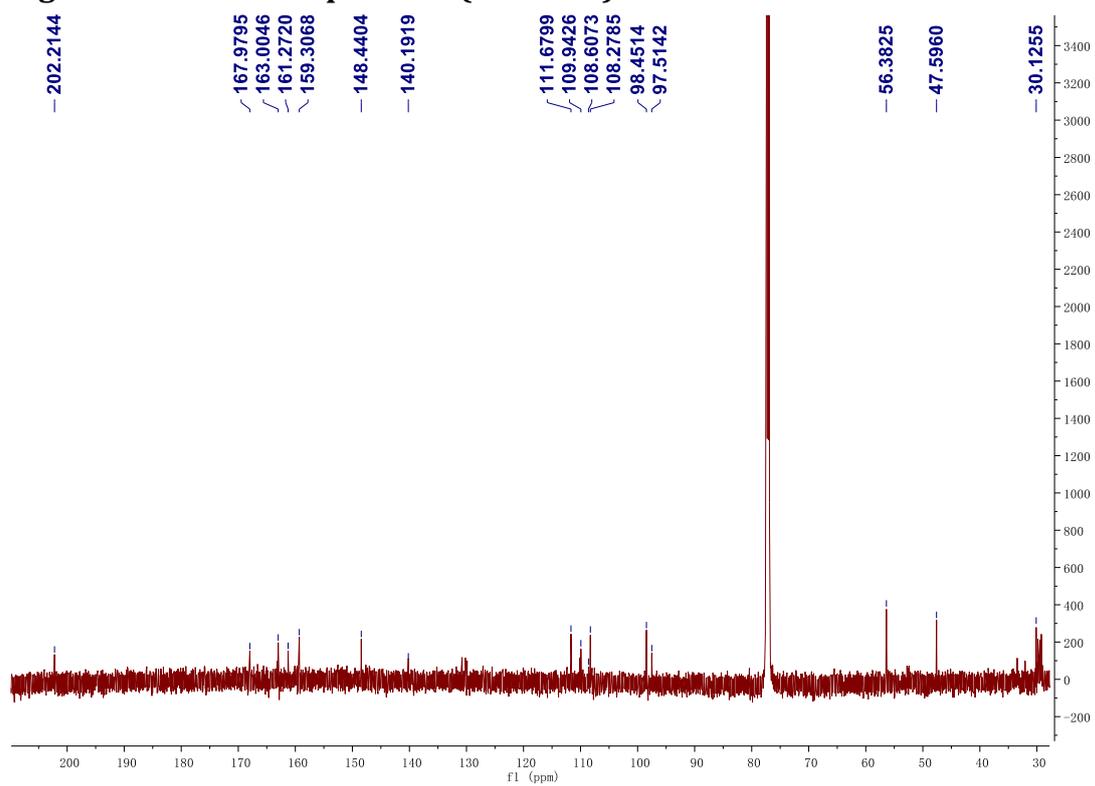
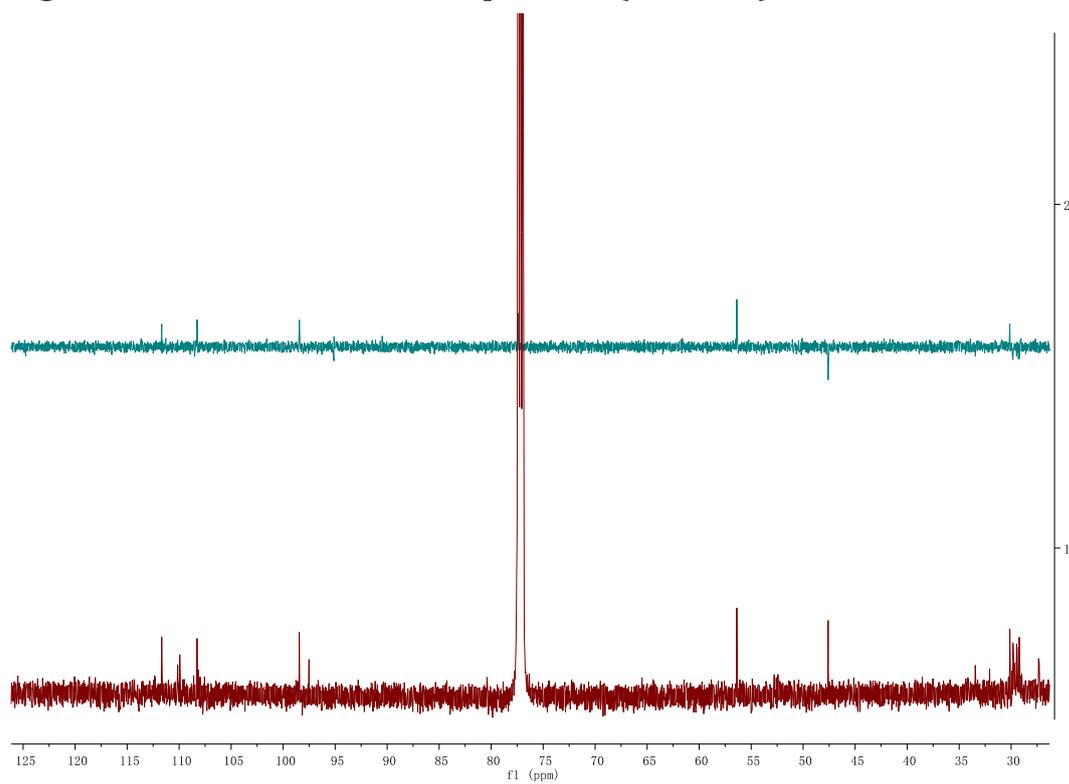


Figure S40.  $^{13}\text{C}$  NMR spectrum (125 MHz) of 7 in chloroform-*d*



**Figure S41. DEPT-135  $^{13}\text{C}$  NMR spectrum (125 MHz) of 7 in chloroform-*d***



**Figure S42.  $^1\text{H}$ - $^1\text{H}$  gCOSY NMR spectrum (500 MHz) of 7 in chloroform-*d***

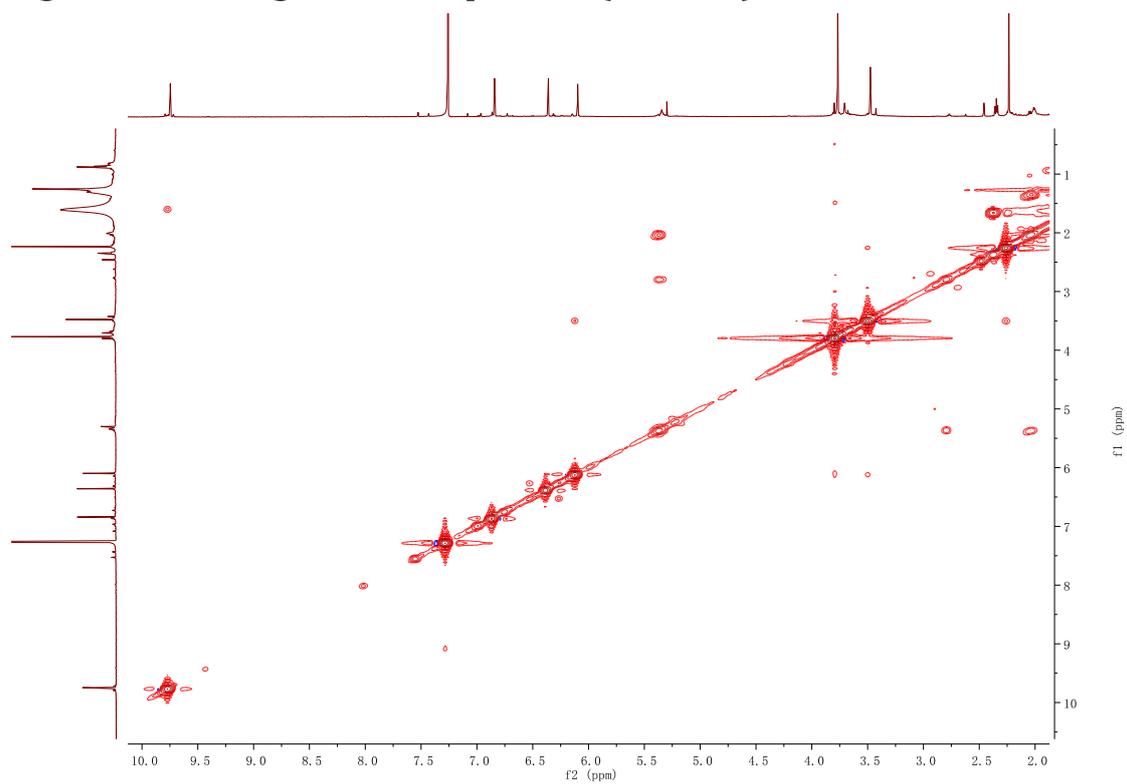
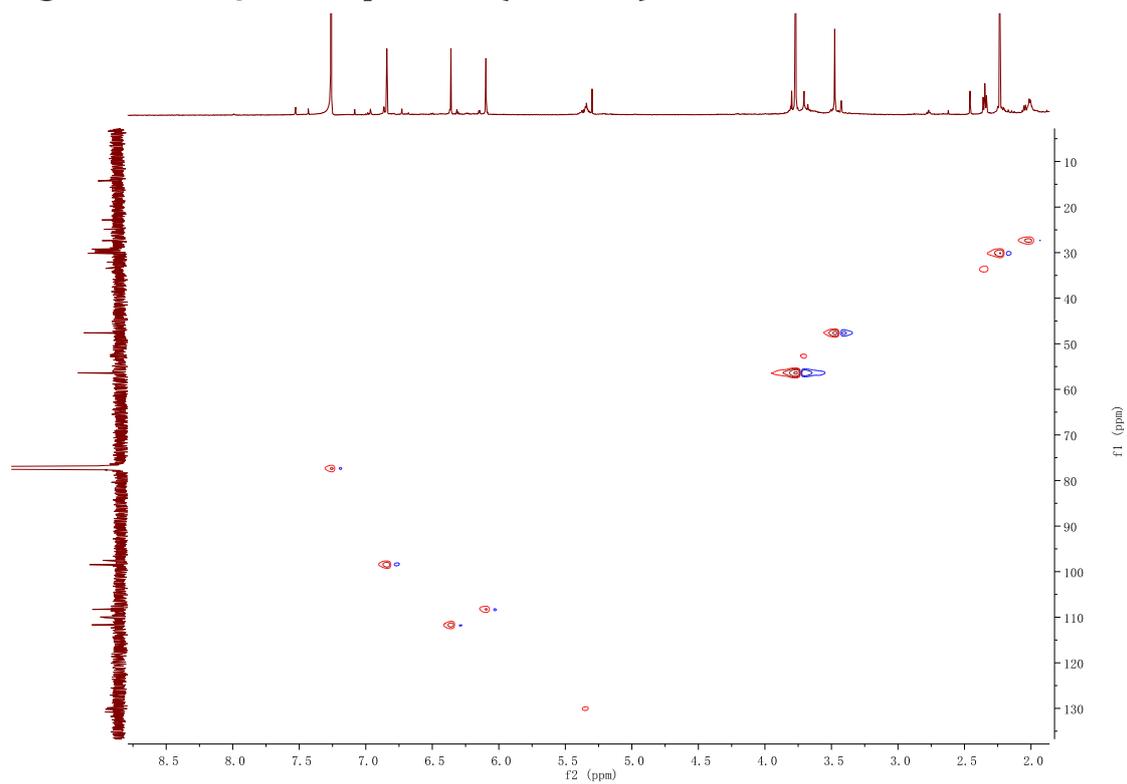


Figure S43. HSQC NMR spectrum (500 MHz) of 7 in chloroform-*d*



**Figure S44. HMBC NMR spectrum (500 MHz) of 7 in chloroform-*d***

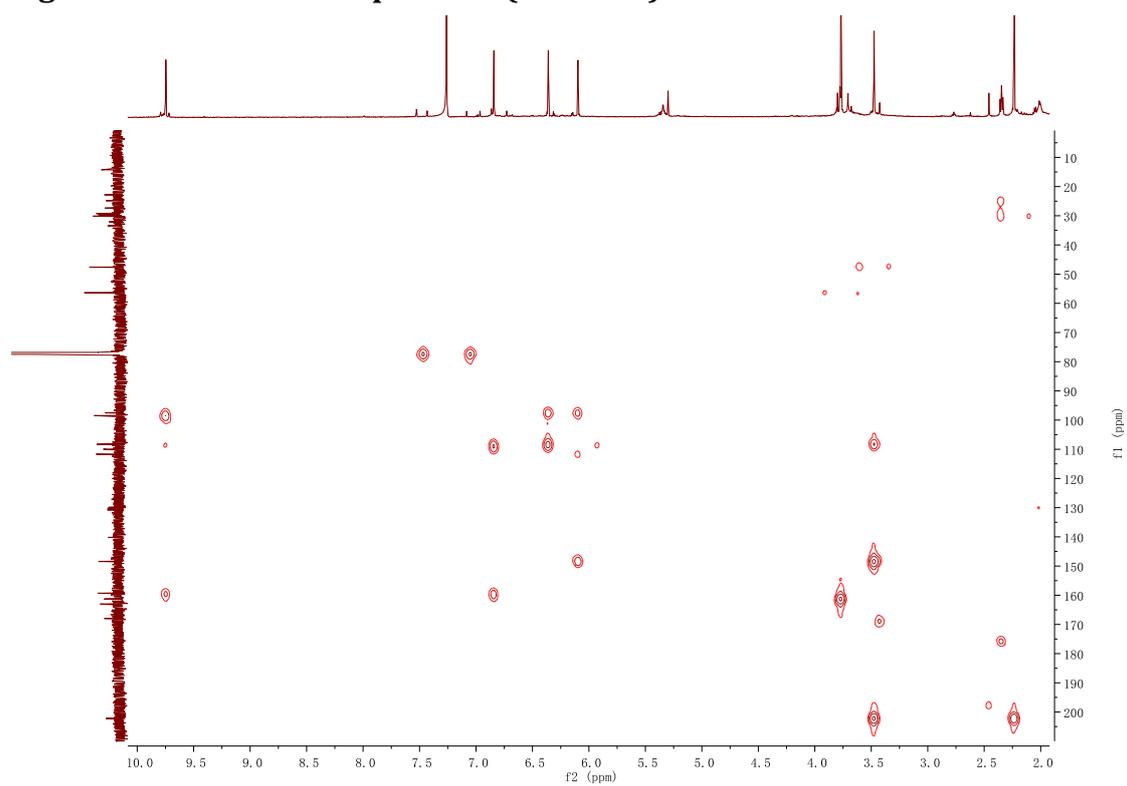


Figure S45. <sup>1</sup>H NMR spectrum (600 MHz) of 8 in chloroform-*d*

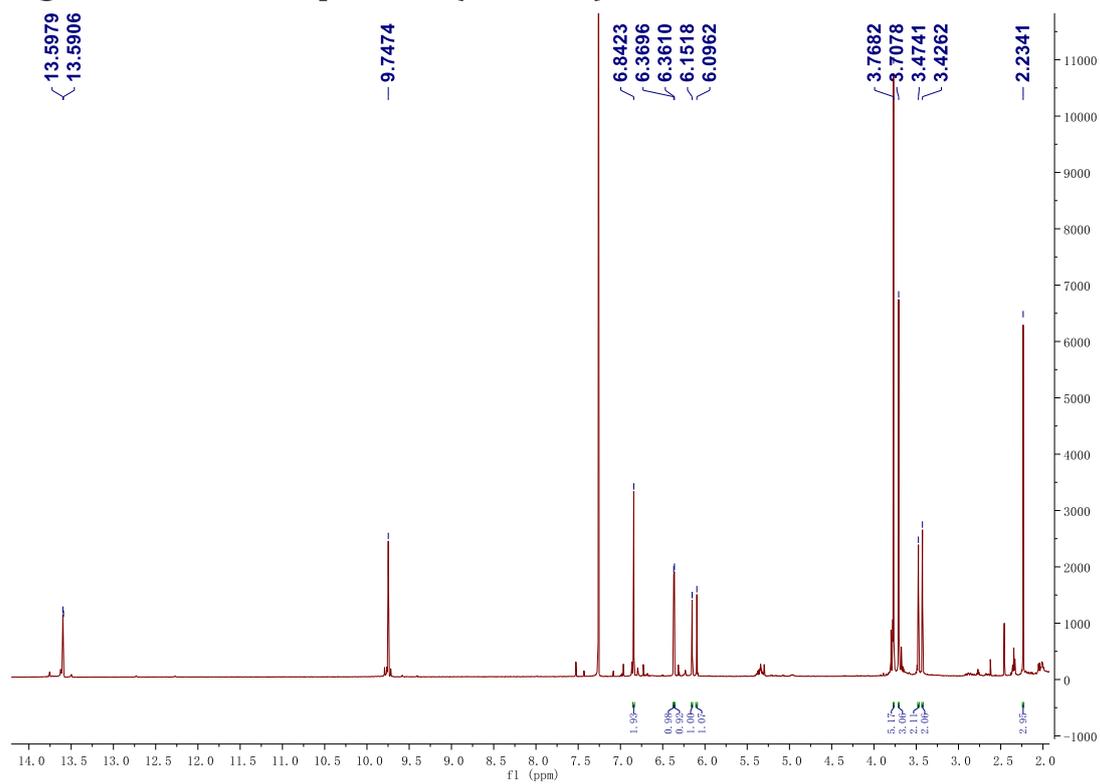
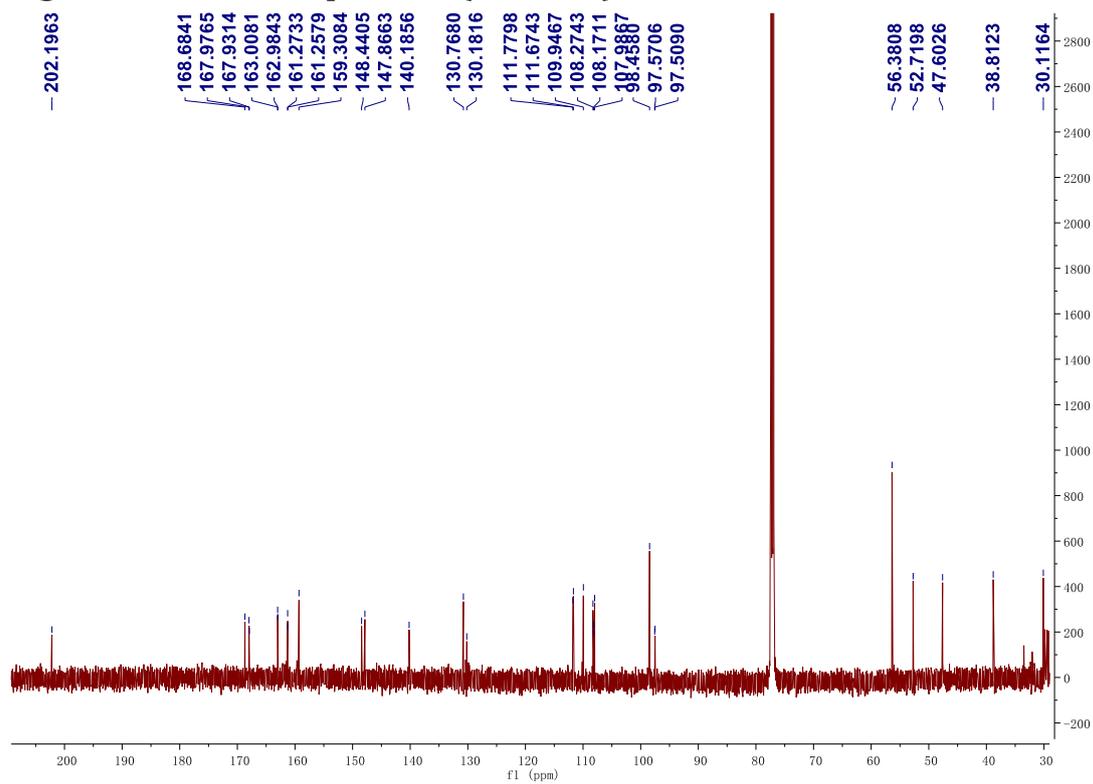
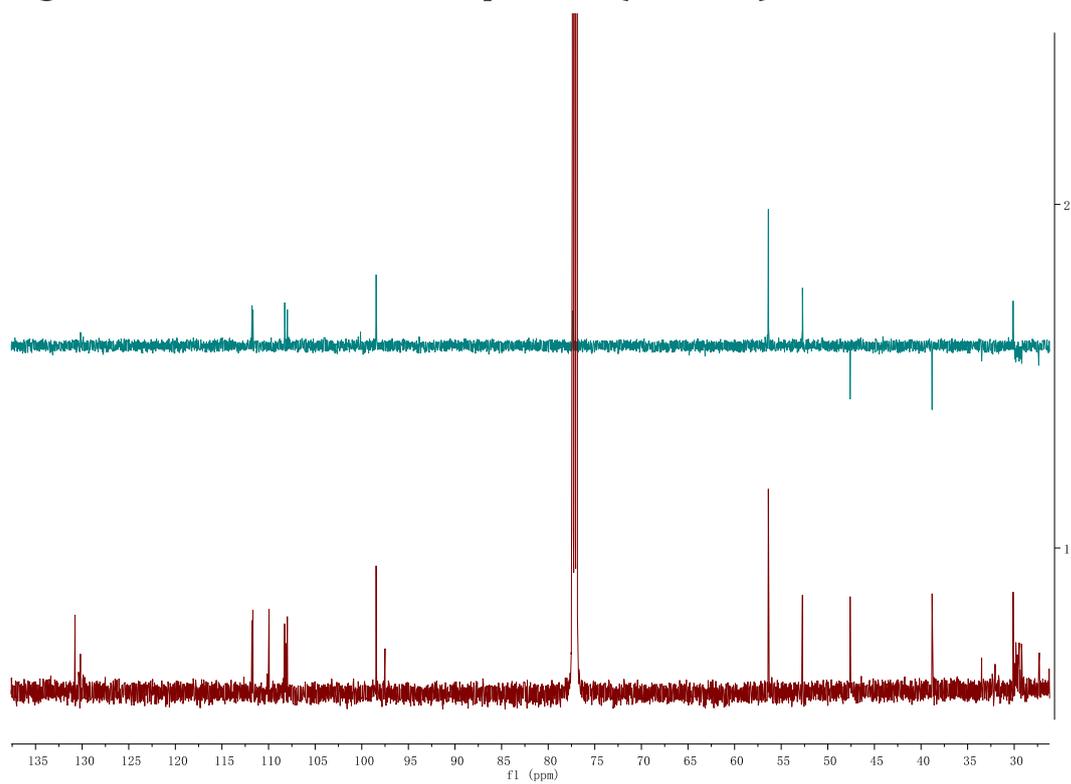


Figure S46. <sup>13</sup>C NMR spectrum (150 MHz) of 8 in chloroform-*d*



**Figure S47. DEPT-135  $^{13}\text{C}$  NMR spectrum (150 MHz) of 8 in chloroform-*d***



**Figure S48.  $^1\text{H}$ - $^1\text{H}$  gCOSY NMR spectrum (500 MHz) of 8 in chloroform-*d***

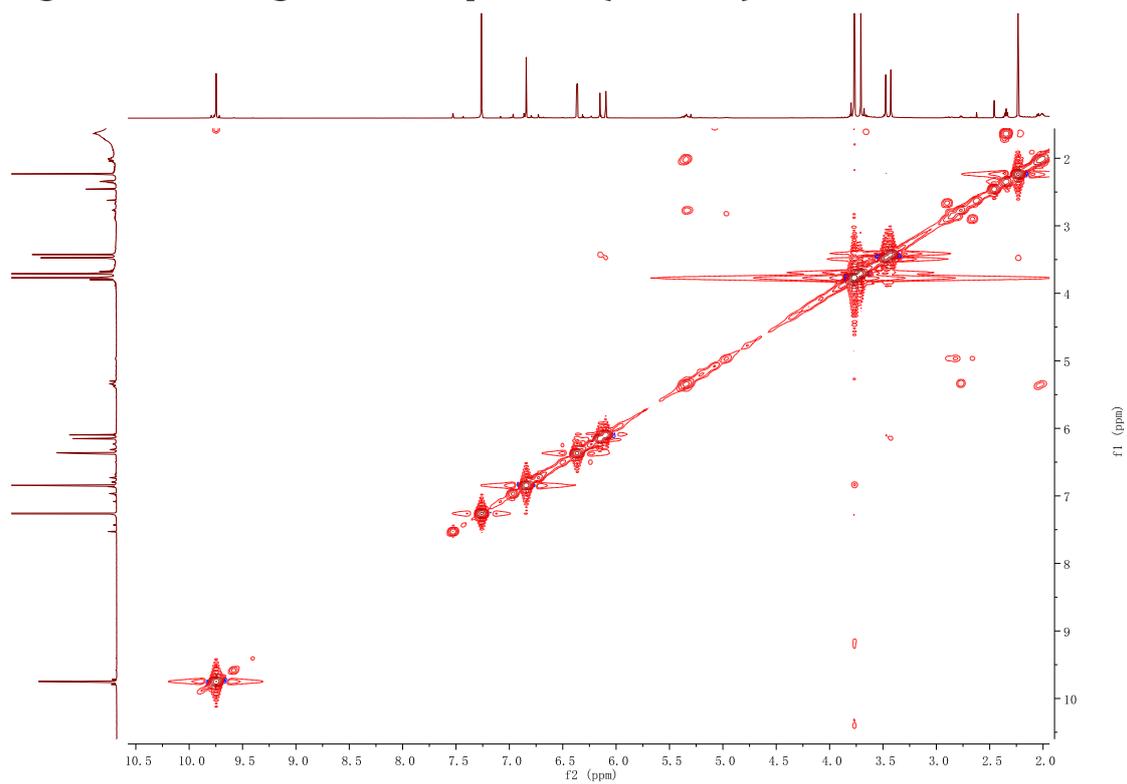


Figure S49. HSQC NMR spectrum (600 MHz) of 8 in chloroform-*d*

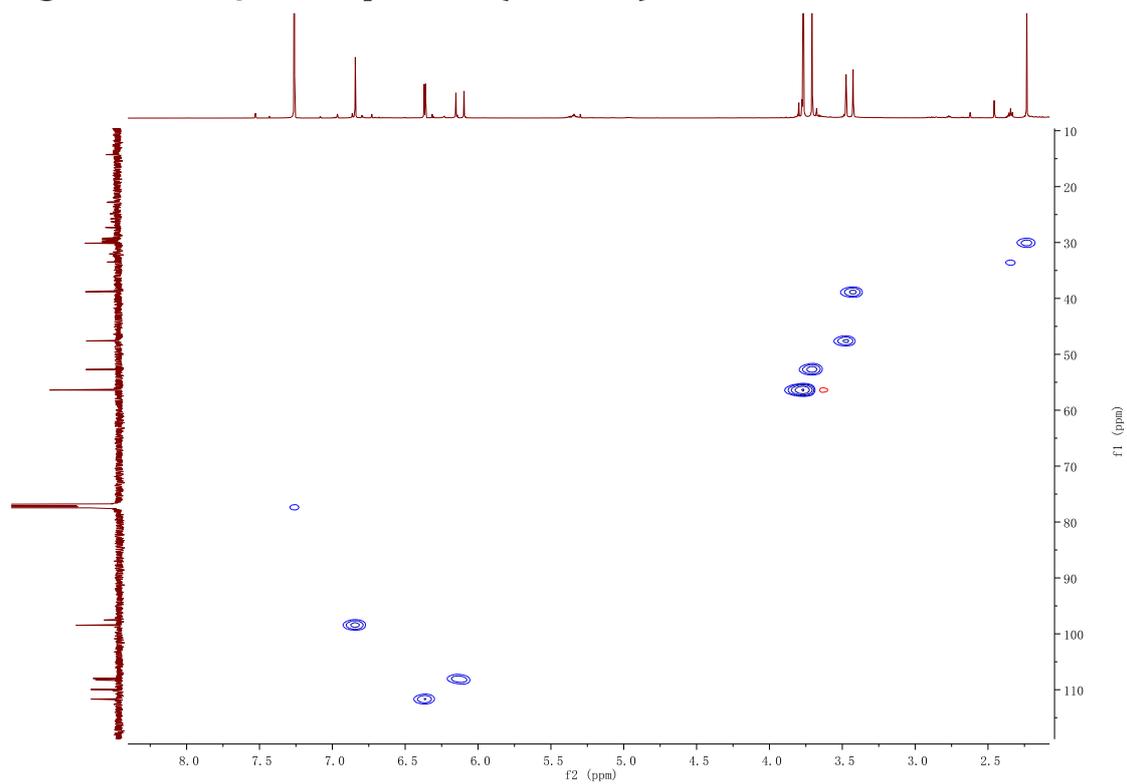


Figure S50 HMBC NMR spectrum (600 MHz) of 8 in chloroform-*d*

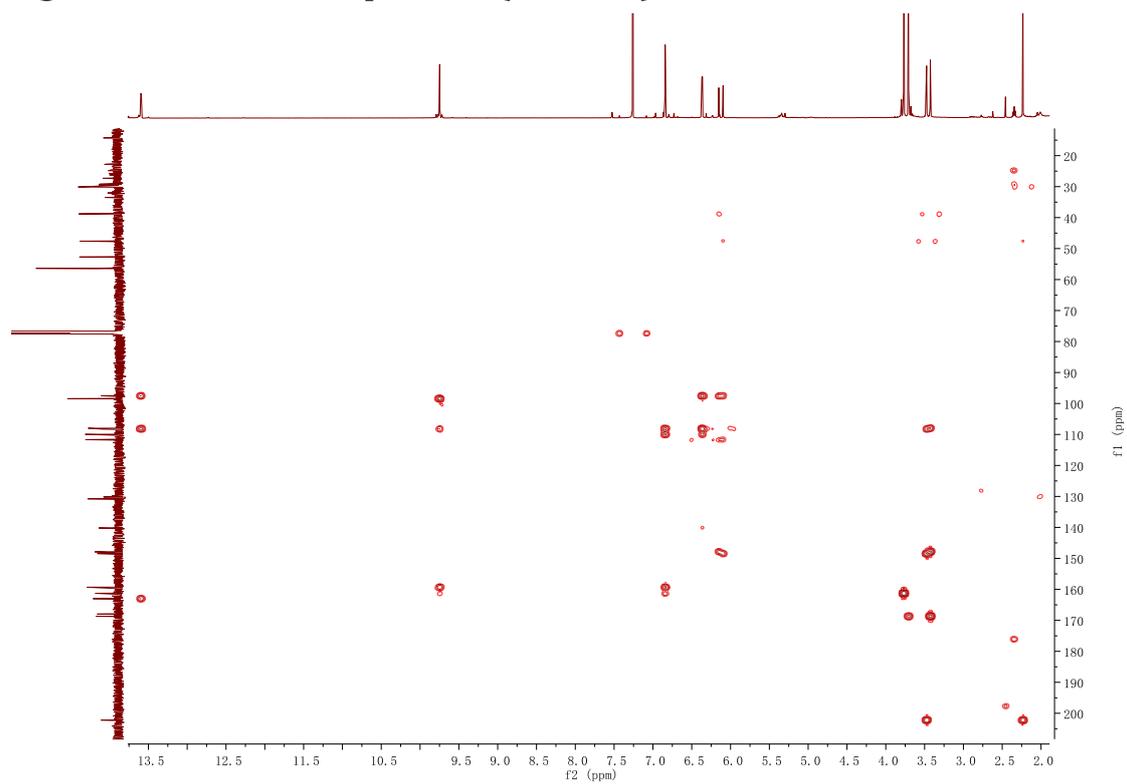


Figure S51.  $^1\text{H}$  NMR spectrum (500 MHz) of 9 in chloroform- $d$

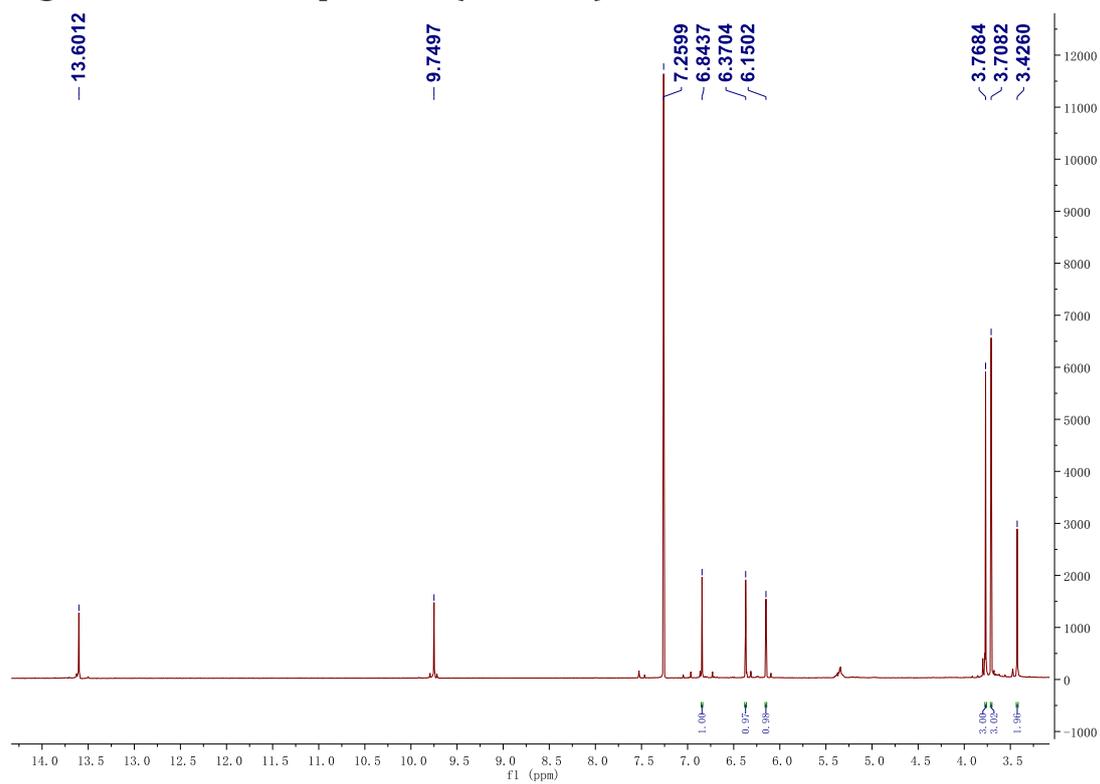
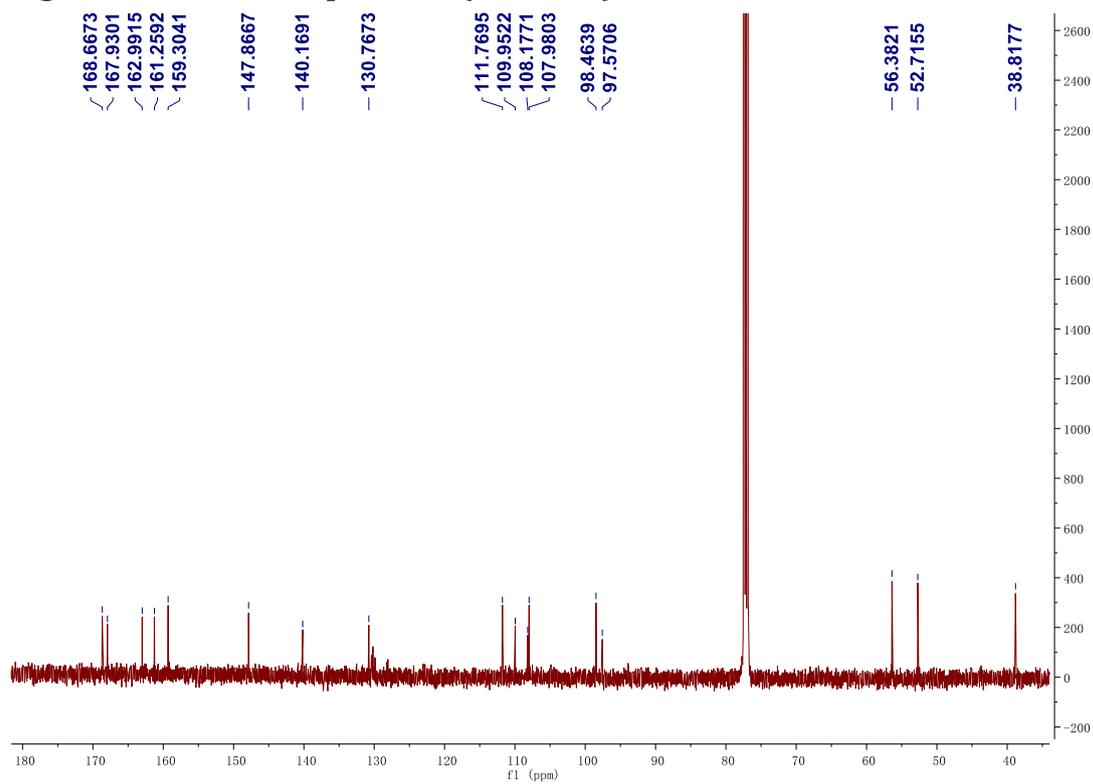
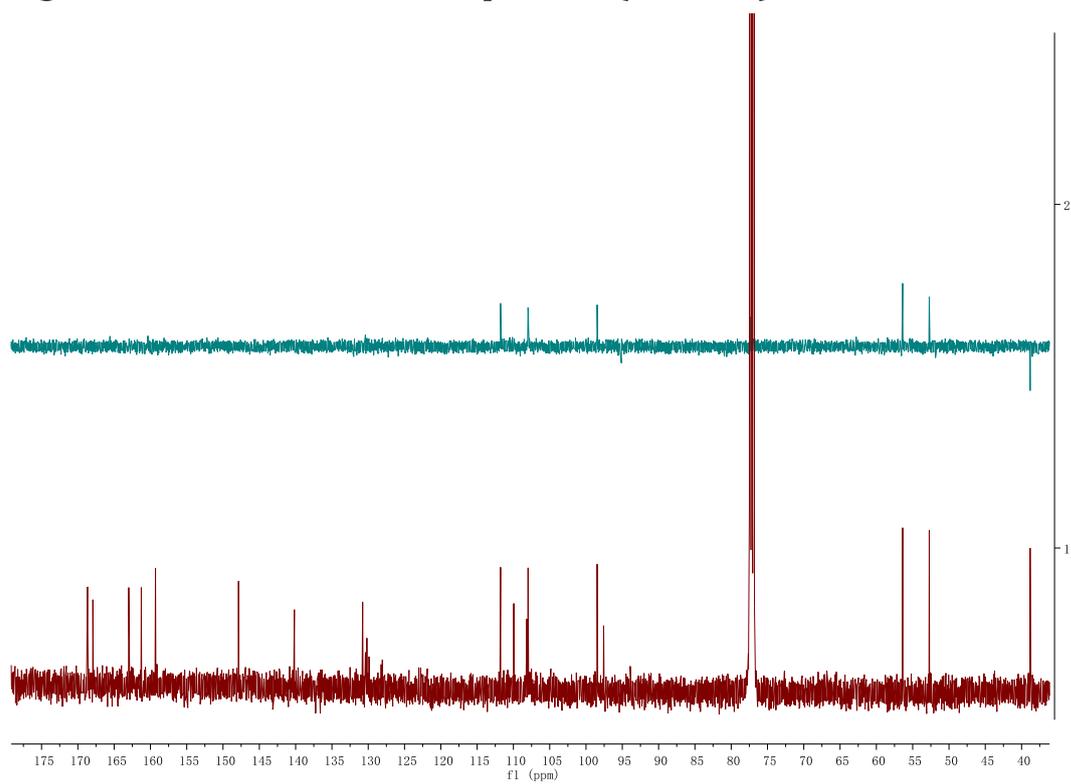


Figure S52.  $^{13}\text{C}$  NMR spectrum (125 MHz) of 9 in chloroform-*d*



**Figure S53. DEPT-135  $^{13}\text{C}$  NMR spectrum (125 MHz) of 9 in chloroform-*d***



**Figure S54.  $^1\text{H}$ - $^1\text{H}$  gCOSY NMR spectrum (500 MHz) of 9 in chloroform-*d***

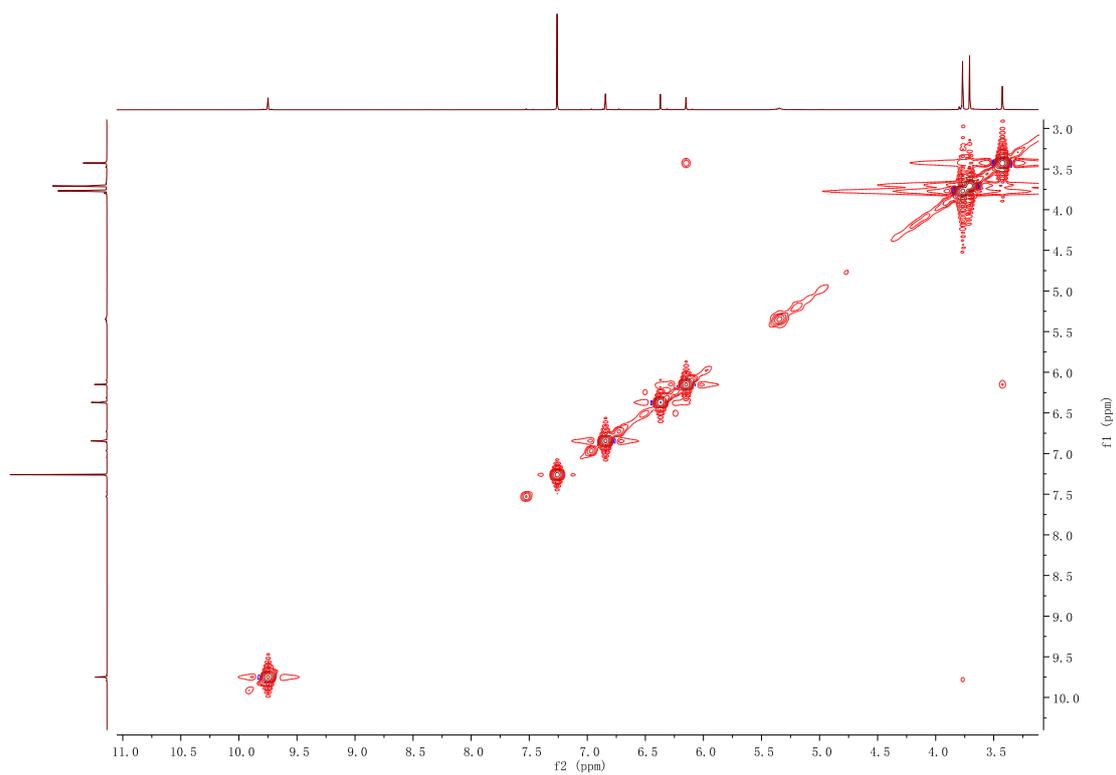
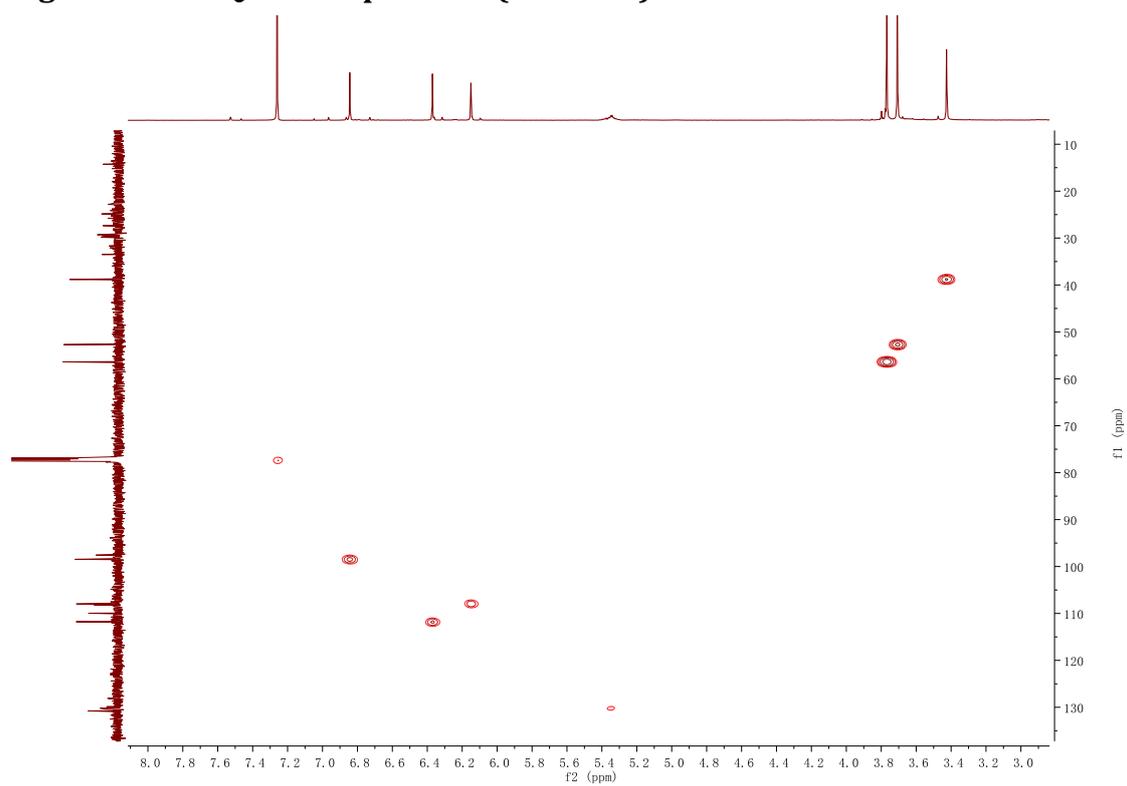


Figure S55. HSQC NMR spectrum (500 MHz) of 9 in chloroform-*d*



**Figure S56. HMBC NMR spectrum (500 MHz) of 9 in chloroform-*d***

